

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 118973

TO: Jennifer Graser_

Location: 3b09/3c18

Wednesday, April 07, 2004

Art Unit: 1645 Phone: 272-0858

Serial Number: 09 / 844281

From: Jan Delaval

Location: Biotech-Chem Library

Rem 1A51

Phone: 272-2504

jan.delaval@uspto.gov

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STIC-Biotech/ChemLib

From:

Hutzell, Paula

Sent:

Wednesday, April 07, 2004 3:01 PM Graser, Jennifer, STIC-Biotech/ChemLib

To: Subject:

RE: rush search

approved

----Original Message-----From:

Graser, Jennifer

Sent:

Wednesday, April 07, 2004 12:26 PM Hutzell, Paula

To:

rush search

Subject: Importance: High

Hi Paula,

Could you please authorize the following rush search for an amendment which is due?

Thanks, Jennifer

STIC:

Please search SEQ ID NO: 1 from 09/844,281 in pending and commercial databases.

Thanks, Jennifer Graser REMSEN EO3 B09/ 3C18 mailbox AU 1645 272-0858



Searcher:	an
Phone:	22504
Location:	
Date Picked Up:	4 tr " "
Date Completed:	417
Searcher Prep/Revi	ew:
Clerical:	(0
Online time:	1.0

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
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VENDOR/COST (where applic.	.)
STN:	_
DIALOG:	_
Questel/Orbit:	_
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (specify):	_

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

April 7, 2004, 17:29:55 ; Search time 18 Seconds (without alignments) 2409.691 Million cell updates/sec Run on:

Title: Perfect score:

US-09-844-281-1 4202 1 AGKSFPDVPAGHWAEGSINY.....ITSEIGSQAVHVNVLNNPNL 833

Scoring table:

Sequence:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	bacillus an	bacil	baci		baci	acetogen	bacillus s	1 escherichia	escherichi	brevibacil	r outer m	ğ	r outer	escherichi	7 escherichia	7 r outer mem	9 drosophila					r outer	lactobac	ricketts	O thermus the	4 staphylococ	7 salmonella	9 chlamydia p	6 t amylopull	6 proteus mir	clostridi	rickettsi	drosophi
Descr	P94217	P4905;	P4905	O9rmz()	P3853,	P22251	P1942	P3205:	P3366	P3853(Q9kka:	P0654	B696d	P7634'	,^8×8¢	Q5304°	18A60	05302	P3582'	P1532	P38058	00665	00247	P1491,	P3583(Ø2365 ⁷	P2592'	6826Ö	P3853(P1646	P3853!	P1592:	CMA60
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SLAP BACST P2P LACLC AIDA ECOLI WSP1_PLAFD MSP1_PLAFD SLAT SLOTM MARA_RICCM M	
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ALIGNMENTS

RESU	RESULT 1			
SLAZ	SLAZ BACAA ID SLAZ BACAA	STANDARD;	PRT;	862 AA.
AC	P94217;			
ď	28-FEB-2003 (F	28-FEB-2003 (Rel. 41, Created)	^	
占	28-FEB-2003 (F	Rel. 41, Last se	quence uj	odate)
H	10-OCT-2003 (F	Rel. 42, Last an	notation	update)
DE	S-layer protei	S-layer protein EAl precursor.		
Ν̈́	EAG OR BA0887.			
SO	Bacillus anthi	Bacillus anthracis (strain Ames), and	es), and	
so	Bacillus anthracis.	racis.		
Ö	Bacteria, Firm	nicutes; Bacilla	les; Bac	Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
ŏ	NCBI TaxID=198094, 1392;	3094, 1392;		
RN	[1]			
RP	SEQUENCE FROM N.A.	N.A.		
RC	STRAIN=Ames;			
ΚX	MEDLINE=226084	MEDLINE=22608414; PubMed=12721629;	1629;	
RA A	Read T.D., Pet	cerson S.N., Tou	rasse N.	Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA	Nelson K.E., 1	rettelin H., Fou	ts D.E.,	Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA BA	Holtzapple E.	K., Okstad O.A.,	Helgaso	Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA	Kolonay J.F.,	Beanan M.J., Do	dson R.J	., Brinkac L.M., Gwinn M.,
RA	DeBoy R.T., Ma	adpu R., Daugher	Ey S.C.,	Durkin A.S., Haft D.H.,
R.A	Nelson W.C., I	Peterson J.D., P.	op M., K	nouri H.M., Radune D.,
RA	Benton J.L., N	Mahamoud Y., Jia	ng L., H	ance I.R., Weidman J.F.,
æ	Berry K.J., Pl	laut R.D., Wolf	A.M., Wa	ckins K.L., Nierman W.C.,
æ	Hazen A., Clir	ne R., Redmond C	., Thwai	Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
æ	Thomason B., i	Friedlander A.M.	, Koehle	Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto AB.,

and comparison to Bacillus anthracis pactersa."; (2003). "The genome sequence of closely related bactersa Nature 423:81-8\$ (2003). Fraser C.M.;

SEQUENCE FROM N.

SEQUENCE recomment of 131;
MEDLINE-Stein (1913);
MEDLINE-9726011; PubMed-9106206;
Mesnage S., Tost-Couture B., Mock M., Gounon P., Fouet A.;
Molecular characterization of the Bacillus anthracis main S-layer component: evidence that it is the major cell-associated antigen.";
Mol. Microbiol. 23:1147-1155(1997).
I- FUNCTION: The S-layer is a paracrystalline mono-layered assembly of proteins which coat the surface of bacteria.
SINGELULAR LOCATION: Cell wall.
I- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
This produced through a collaboration of the surface of through a collaboration.

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EMBL, AE017027; AAP24884.1; -. EMBL, X99724; CAA68063.1; -. TIGR, BA0887; --INCEFFC; IPRO01119; SLH.

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0; Mismatches 0;
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Best Local Similarity 100.
Marches 833; Conservative
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MEDINE=97082955; PubMed=8964497;
MEDINE=97082955; PubMed=8964497;
MEVELY., MeVelgh R.R., Malathi P., Ghosh B.K.;
"The complete nucleotide sequence of the Bacillus licheniformis NM105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGKSFPDVPAGHWAEDSINYLVDKGAIVGKPDGTYGPTESIDRASAAVIFTKILNLPVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 NAQPSFKDAKNLWSSKYIAAVEKAGVVKGDGKDNFYPEGKIDRASFASMLVGAYNLKEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGKSFPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDNAQAYVTDVKVSEPTKLTLTGTGLDKLSADDVTLEGDKAVAIEASTDGTSAVVTLGGK
                                                                                                                                                                                                                                                                                                               S-layer-encoding gene..., General Series of the Series of Series of Series of Series of Series of Series of Protection: which coat the surface of bacteria.

-!- FURCATION: The S-layer is a paracrystalline mono-layered assembly of proteins which coat the surface of bacteria.

-!- SUBCELIULAR LOCATION: Cell wall.

-!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                     Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFADCA4FF27D32AF CRC64;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
S-layer protein precursor (Surface layer protein)
Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.4%; Score 2833.5; DB 1; 67.3%; Pred. No. 3.6e-116; ive 98; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
S-LAYER PROTEIN.
SLH 1.
SLH 2.
SLH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat
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155 SLF
217 SLF
92734 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U38842; AAC44405.1; -. PIR; JC4930; JC4930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; UC4930.
Pfam; PF00395; SLH; Signal; Cell wall; S-layer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            874 AA;
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                                                                                                                                                                                               FROM N.A.
                                                                                                                                                  NCBI_TaxID=1402;
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Best Local Simi:
Matches 569;
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----KKDNAQAYVT---DVKVSEPTKLTLTGTGLDKLSADDVTL----EGDKAVA1EA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGKSFPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 AGKTFPDVPADHWGIDSINYLVEKGAVKGNDKGMFEPGKELTRAEAATMMAQILNLPIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NAOPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGELVITFEDLID-HWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 NGTPATKFKDLETLNWGKEKANILVELGISVGTGDQWEPKKTVTKAEAAQFIAKTDKQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 TEAAKVESAKAVTTOKVEVKFSK-----AVEKLTKEDIKVTNKANNDKVLVKEVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAFKLNDEKGNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATSTTGKLAVGIKQGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 LOFTVKDENGTEVV----SPEGIEFV-----TPA-----AEKINAKGEITLAKGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSONLVVGEKASLNKLVATIAGEDKVVDPGSISIKSSNH--GIISVVNNYITAEAAGEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 NNK-VYEGDNAYVQ---VELKDOFNAVTTGKVEYESLNTEVAVVDKATGKVTVLSAGKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514 PFGANTAAIKEVLPKTG-VVAEGGLDVVTTDSGSIGTKTIGVTGNDVGEGTVHF--QNGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STDGTSAVVTLGGKVAPNKDLTVKV----KNQSFVTKFVYEVKKLAVEKLTFDDDRAGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVEVQVTKRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 LTIKVGD------VTKDVKFKV-TTDSRKLVSVKANPDKLQVVQNKTLPVTFVTTDQYGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229; Conservative 126; Mismatches 302; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C1638D26A1C6B101 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           S-LAYER PROTEIN SAP.
SLH 1.
SLH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 719; DB 1;
Pred. No. 2.3e-24;
                                                                                                                                                                                                                                                                                                                        Interpro; IPR003343; Big_2.
Interpro; IPR008964; Invasin_intimin.
Interpro; IPR001119; SLH.
Bacteriol. 177:614-620(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                           814
93
154
213
86620 MM;
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Pfam; Pr02368; Big_2; 1.
Pfam; PF00395; SLM; 3.
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EMBL; Z36946; CAA85408.1; -
PIR; 140048; I40048.
TIGR; BA0885; -
                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Glycoprotein;
SIGNAL 1
CHAIN 30 814
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94 1
155 2
814 AA;
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                                                                                     SERVING IN STEHKVRIVDEGTEGGKVYLDRNDNATFDGNDVALGYVTAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                ELEKSNLDDIVKGINLTKETQHKVRVVKSGAEQGKLYLDRNGDAVPNAGDVKLGDVTVSQ
                                                                 RKEVSVKANPDKLQVVQNKTLPVTFVTTDQYGDPFGANTAAIKEVLPKTGVVAEGGLDVV
                                                                                                                                                                                                                                  AGQKGEAADT--TLGAGNTVAYQLSNYTTEGVYADAADLAGYEFRVGNDKIASAKIEGKT
                                                                                                                                                                                                                                                                      VVVTGKTPGKVDIHLTKNGATAGKATVEIVQETIAIKSVNFKPVQTENFVEKKINIGTVL
                                                                                                                                                                                                                                                                                                                                                                                                              TSDSA-----LPNF----KADLYDTLTTKYTDKGTLVFKVLKDKDVITSEIGSQA
TIAGEDKVVDPGSISIKSSNHGIISVVNNYITAEAAGEATLTIKVGDVTKDVKFKVTTDS
                    TTDSGSIGTKTIGVTGNDVGEGTVHFONGN--GATLGSLYVNVTEGNVAFK--NFELVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1996 [Rel. 33, Created)
1996 [Rel. 33, Last sequence update)
1902 [Rel. 42, Last amotation update)
Protein sap precursor (Surface layer protein) (Surface array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence of Bacillus anthracis Ames and comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mock M., Fouet A.; S-layer: cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 30-40; 209-218; 281-291
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NCBI_TaxID=198094, 1392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95138020; PubMed=7836294;
Etienne-Toumelin I., Sirard J., Duflot E., M
"Characterization of the Bacillus anthracis
sequencing of the structural gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      814
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Bacillus anthracis (strain Ames), and
Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22608414; PubMed=12721629;
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STRAIN=Sterne,
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STRAIN=Ames;
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-!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly of proteins which cost the surface of bacteria.
- SUBCELLULAR LOCATION: Cell wall.
- PTM: PROBABLY GLYCOSYLATED.
- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
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SEQUENCE FROM N.A.
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ID SLAP BAN
AC P38537;
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GATLGSLYVNVTEGNVAFKNFELVSKVGQYGQSPDTKLDLNVSTTVEYQLSKYTSDRVYS 630
                                                                                                                    ---RGLEKELDKYVTEENOK 619
                                                                                                                                                                         -----IHLTKNGATA 678
                                                                                                                                                                                                                   620 NAMTVSVLPVDANGLVLKGABAAELKVTTTNKEGKEVDATDAQVTVQNNSVITVGQGAKA 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SNOO646; Ami 3; PROSITE; PROOF46; Ami 3; PROSITE; PSO1072; Ami 3; PROSITE; PSO1072; Ami 3; PROSITE; PSO1072; Ami 3; Prochetical protein; Hydrolase; Cell wall; Repeat; S-layer; Signal; Plasmid. 1 26 POTENTIAL.
                                                                                                                                                                                                                                                                     GKA-TVEIVQETIAIKSVNFKPVQTENFVEKKINIGTVLELEKSNLDDIVKGINL 732
                                                                                                                                                                                                                                                                                                     680 GETYKVTVVLDGKLITTHSFKVVDTAPTAK----GLAVEFTSTSLKEVAPNADL 729
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HYPOTHETICAL CELL-WALL AMIDASE PXO2-42.
SLH 1.
SLH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okinaka R.T., Cloud K., Hampton O., Hill K.K., Keim P., Lamke G., Kumano S., Manter D., Martinez Y., Svensson R., Tatum L.R., Brown A.E., Jackson P.J.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Cell wall (Potential).
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE NACTYLMURAMOYL-L-ALANINE AMIDASE FAMILY 3.
-!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB_2003 (Rel. 41, Created)
28-FEB_2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical cell-wall amidase pXO2-42 precursor (EC 3.5.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus anthracis.
Plasmid pXO2.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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AMIDASE.
9A171DC4ED05CA78 CRC64;
                                                                                                                                                                         DPENLEGYEVESKNLAVADAKIVGNKVVVTGKTPGKVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                 531 AA
                                                                                                                    581 KEAKATLALEL-KAPGAFSKFEV----
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531 HY
72 SL
132 SL
193 SL
521 AM
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531 AA;
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Matches 158;
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                                                                                                                                                                                                             256
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                                                                                                                                                                                                                                                                                        257 DKWTPLYEKRETI---HSTFTTYPEASHSSKVLGT-----HSPQTVT--VIEEKGSW 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 VRVQKLFAQKTPFTALLTRDAYSRPGKNATDSLGKRVEFAKKNKGDIFVSIHANGFNGNA 423
                                                                                                                                                                                               478
                                           88 KPSFQDAKNHWASPYIAAVEKAGVIYGDGSGNFNPSKDIDRASMASMLVEAYKLNNRIIG
                                                                                                         VQVTKRGGLTVSNTGIITVKNLDTPA----SAIKNVVFALDADNDGVVN-----
QPSFXDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNG
                                                                                                                                                                    183 NAQAYVID---VKVSEPIKLILIGIGLDKLSADDVILEGDKAVAIEASIDGISAVVI-LG
                                                                                                                                                                                                                                                      239 GKVAP--NKDLTVKVKNQSFVT--KFVYEVKKLAVEKLTFDDDRAGQAIAFKLNDEKG--
                                                                                    ELVITTEDDILDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bowditch R.D., Baumann P., Yousten A.A.;
"Cloning and sequencing of the gene encoding a 125-kilodalton
"Cloning and sequencing of the gene encoding a 125-kilodalton
surface-layer protein from Bacillus sphaericus 2362 and of a related
curptic gene.";
J. Bacteriol. 171:4178-4188(1989).
-!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
of proteins which coat the surface of bacteria.
-!- SUBCELLULAR LOCATION: Cell wall.
-!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 HGTETPYYKAPTQKSNPYVNDSRILAEKIQ-KRLITALQTRDRGVKIGNLYVLREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----YGSKISGKDFALNSQNLVVGEKASLNKLVATIAGEDKVVDPGSISIKSSN
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R PIR; A3886; A38866.

R InterPro; IPR00119; SLH.

DR Pfam; PF00395; SLH; 3.

DR PROSTIE; PS01072; SLH DOMAIN; 2.

EWBL; PS01072; SLH DOMAIN; 2.

EWBL; PS01072; SLH DOMAIN; 2.

DR PROSTIE; PS01072; SLH DOMAIN; 2.

EWBL; SCH SLH STREATER 125 KDA PROTEIN.

31 1176 SLH 1.

32 151 SLH 2.

151 SLH 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus sphaericus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Surface-layer 125 kDa protein precursor.
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                                                                                                                                                                                                                                                                              283 IAFKLNDEKGNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATSTTGKL-----AVG 336
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                                                             71
                                                                                   66
                                                                            42 YAKEAVQSLVDAGVIQGDANGNFNPLKTISRAEAATIFTNALELEAEGDV--NFKDVKAD
                                                                                                                     .00 AWYYDAIAATVENGIFEGVSATEFAPNKQLTRSEAAKILVDAFELEGE--GDL-SEFADA
                                                                                                                                                                                                                                                  343 ISNVKAGDKEINVKNVEFTAVDNKIPEVTE-----VKSLGTKAVKVTLSEPVENLSSTNF
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                                                                                                       72 IWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMIVSAYNLKDKVNGELVTTFED-
                                                                                                                                                  131 -LLDHWGEEKANILINLGISVGT--GGK--WEPNKSVSRAEAAQFIALTDKKYGKKDNAQ
                                                                                                                                                                                          .86 AYVIDVKVSEPTKLTLTGTGLDKLSADDVTLEGDKAVAIEAST-----DGTSAVVTLGG
                                                                                                                                                                                                                                     240 KVAPNK--DLTVKVKNQSFVTKFVYEV-------KKLAVE-KLTFDDDRAGQA
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                                                             13 WAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDENAQPSFKDAK-N
                                                                                                                                                                     157 STVKPWAKSYLEÍAVANGVIKGSEANGKTNLNPNAPITRODFÁVVFSRT------
                                                                                                                                                                                                                                                                                                                                                                                     398 TLDGKAYFGNVVMGAGNKTVILTPYSSSALSVGDHKLTVSGAKDFAGFVSLNSTHEFKVV
                                          Gaps
                                          236; Conservative 123; Mismatches 307; Indels 310;
                     Length 1176;
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125225 MW; 1A9A458EF433788C CRC64;
                    8.3%; Score 348; DB 1; 24.2%; Pred. No. 4.7e-08;
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 1176 AA;
                              Similarity
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J. Bacteriol. 176:1224-1233(1994).

J. Bacteriol. 176:1224-1233(1994).

J. PUNCTION: The S-layer is a paracrystalline mono-layered assembly of proteins which coat the surface of bacteria.

J. SUBCELLIDIAR LOCATION: Cell wall. This bacterium is covered by a Slayer with hexagonal symmetry.

J. PTM: THE CARBOHYDRATE CONTENT OF THIS PROTEIN IS ABOUT 8% WHICH CORRESPOND TO ABOUT 40 TO 50 SUGAR MOLECTIES PER MONOMER. O-LINKE GLYCANS CONSIST OF GL., GALINAC AND GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90036724, PubMed=2681162;
Peters J., Peters M., Lottspeich F., Baumeister W.;
S-layer protein gene of Acetogenium kivui: cloning and expressi
Bscherichia coli and determination of the nucleotide sequence.",
J. Bacteriol. 171:6307-6315(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92281680, PubMed=1596358;
Peters J., Rudolf S., Oschkinat H., Mengele R., Sumper M.,
Kellermann J., Lottspelch F., Baumeister W.;
"Bydence for tyrosine-linked glycosaminoglycan in a bacterial
surface protein."
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                                                                                                                                                                                             Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
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Glycoprotein; Repeat; Cell wall; S-layer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE, AND CARBOHYDRATE-LINKAGE SITES.
STRAIN=DSM 2030;
                                                    01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
Cell surface protein precursor (S-layer protein)
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SER/THR-RICH.
SER/THR-RICH.
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Biol. Chem. Hoppe-Seyler 373:171-176(1992)
762
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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   STANDARD;
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PROSITE; PS01072; SI
                                                                                                                                                                           Acetogenium kivui.
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   SLAP ACEKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKVTTDS-----RKLVSVKANPDKLQV---VQNKTLPVTFVTTDQYGDPFGANTAAIK 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSSASYKADAKVITEGSTTY-----YITDNTVLIN-NTSDGYKALKLID--- 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKDATNL-NVKIVADNYNVAKVVVFNNASFVSTTTSTVXAYVTGTADVYV--NGSTFTRL 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVEIVOETIAIKSVNFKPVQTENFVEKKINIGTVLELEKSN--LDDIVKGINLIKETQHK 739
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                                                                                                                                                                                                                                                        176 -VIKRGDLALILDRALE-VPMVKYVDGKEVLGEPLISKVATKAEYTVIAINAQDRSVEEG 233
                                                                                                                                                                                                                                                                                                                                             STIGKLAVG---IKQGDYKVEVQV------TKRGGLIVSNIGIIIVKNLDIPAS 372
                                                                                                                                                                                                                                                                                                                                                                     FIEGDSVGTTVYKNDDNKTAIKVDDNAYVLYNGYLTKVSKVTVKEGAEVTIIN----- 338
                                                                                                                                                                                                                                                                                                                                                                                                AIKNVVFALDADNDGVVNYGSKLSGKDFALNSQNLVVGEKASLNKLVATIAGEDKVVDPG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IKANDYIYYGKOYDVNGNVVGTVİYVRNQVİ----GTVTEKSVSGSTYKASIDNVS 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTVADNNVWNQLEPGKKVTVILNKDNVIVGISSTTTTTAVNYAIFKEKSDPFTAWFAKVK 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502 LILPD---AAEKVFDAVYSDVYDKVNLAEGTIVTYTVDANGKLNDI-----QRANDQP 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574 LGSLYVN-----VTEGNVAFFONFELVSKVGQYGQSPDTKLDLNVSTTVEYQLSKYTSDRV 628
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                                                                                                                                A---SFASMLVSAYNLKDKVNGELVTTFEDL-LDHWGEEKANILINLGISVGTG-GKWEP 158
                                                                                                                                                                                                                                                                                         --LIFEDEDRAGQAIAFKINDEKGNADVEYINLANHDVKFVANNLDGSPANIFEGGE--AT 327
                                                                                                                                               70 AQMITFVNRMLGYEDLAEMAKSE-KSAFKDVPQNHWAVGQINLAYKLGLAQGVGNGKFDP
                                                                                                                                                                                  159 NKSVSRAEAAQFI--AL---TDKKYGKKDNAQAYVTDVKVSEPTKLTLTGTGLDKLSAD
                                                                                                                                                                                                          129 NSELRYAQALAFVLRALGFKDLDWPYGYLAKAQ----DLGLVHGLNLAYNG------
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                                                                             47 AVIFTKILNLPVDENAQPSFKDAKNIWSSKYIAAVEK---AGVVKGDGKENFYPEGKIDR
                                                                                                      15 ALVĖSA----MAVGFAATTPFTDVKD--DAPYASAVARLYALNITNGVGDPKFGVDQPVTR
                                                     Gaps
                                                    193;
                         DB 1; Length 762;
                         tch
al Similarity 22.7%; Score 265.5; DB 1; Length 7
al Similarity 22.7%; Pred. No. 0.0001;
193; Conservative 116; Mismatches 347; Indels
34EC9C784DECA67E CRC64;
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GUN BACS6

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STANDARD; FRT; 941 AA

AC P19424;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
82785 MW;
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 762 AA;
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                                                                                                                                                                                     MEDLINE=91037937; PubMed=2230718; Oxamoto K.; Ashkata S., Kawai S., Ito S., Oxamoto K.; Ozaki K., Shikata S., Kawai S., Ito S., Oxamoto K.; Ozaki K., Shikata S., Kawai S., Ito S., Ito S., Oxamoto K.; Ozaki K., Shikata S., Kawai S., Ito S., Oxamoto G. a gene for alkaline cellulase from Bacillus sp. KSM-635."; J. Gen. Microbiol. 136:1327-1334(1990).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311;
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PROSITE; PSO1072; SLH DOMAIN; 2.
Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat;
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10-OCT-2003 (Rel. 42, Last annotation update)
Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 941;
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SIMILARITY: Contains 3 S-layer homology (SLH) domains.
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185 NUCLEOPHILE (BY SIMILARITY).
104628 MW; BEAZAG3B169BFADA CRC64;
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                        Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-gluc
(Alkaline cellulase).
Bacillus sp. (strain KSM-635).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
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SLH 1.
SLH 2.
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PDB; 1G01; 31-DEC-02.
PDB; 1G0C; 31-DEC-02.
InterPro; IPR00180; Gal_bind_like.
InterPro; IPR001879; Gal_bind_like.
InterPro; IPR00119; GIH.
Pfan; PF03424; CBM 17_28; 2.
Pfan; PF00150; callulase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------KTLPVTFVTTDQYGDPFGANTAAIKEVLPKTGVV 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATSPEDNTMSNIILFVGTEDADVISLDNITVSGTEIEVIHDEKGT-ATLPSTFEDGTR 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VAPKNFELVSKVGQ 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               779 QGWDWHTESGVKTALTIEEANGSNALSWEYAYPEVKPSDGWATAPRLDFWKDELVRGTSD 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - IDAENIMYSVHFYTGSHGASHIGYPEGTPSSERSNVMANVRYALDNGVAVFATEWGTSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGMSTHGLQWFGEIVNENAFVALSNDWGSNMIRLAMYIGENGYATNPEVKDLVYBGIELA
                                                     VEKLIF------DDDRAG------QAIAFKLNDEKGNADVEYL--NLANHDVK
                                                                                                                                                                 FVANNLDGSP--ANIFEGGEATSTTGKLAVGI---KQGDYKVEV---QVTKRGGLTVSNTG
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                                                                                                           PEHDMYVIVDWHVHAPGDPRADVYSGAYDFFEEIADHYKDHPKN---HYIIWELANEP--
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
Kiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                               IITVKNL--------AIKNVFALD------
                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDS--RKLVSVKANPDKLQV----VQN-----
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YDEK ECOLI STANDARD; PRT; 1325 AA.
P32051; P76140; P77168;
01-0CT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical lipoprotein ydek precursor (ORFT).
YDEK OR ORFT OR B1510.
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FROM N.A

SEQUENCE FR STRAIN=K12;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 GELVTTFEDLIDHWGEEKANI----LI-----NLG------ISVGTGGKWEPNKSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 PSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASML--VSAYNLKDKVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 WNFLGTGEAFRYIYİGDA------GÖĞELNVSSEĞKVÖSGIITAGMKETGTGNITVKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 NSVITNLGTNIGYDGHGEMNISNQGLVVSNGGSSLGYGETGVGNVSITTGGMWEVNKNV-
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             Alba H., Baba T., Fujita K., Hayahi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takenco K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takenco K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Parorresponding to the 28-0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 595-1325 FROM N.A. MEDDINE=94100243; Pubmed=8274505; Cartwright P.U., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.; Cartwright P.U., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.; M. Bscherichia coli gene showing a potential ancestral relationship to the genes for the mitochondrial import site proteins ISP42 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochim, Biophys. Acta 1153:345-347(1993).
-!- SUBCELLUIAR LOCATION: Attached to the membrane by a lipid anchor
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N-palmitoyl cysteine (Potential).

S.diacylglycerol cysteine (Potential).

N -> K (IN REF. 3).

M -> S (IN REF. 3).
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11 Similarity 19.2%; Pred. No. 0.0073;
210; Conservative 154; Mismatches 367; Indels 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISP42 AND MOM38.
CAUTION: Ref.3 sequence differs from that shown due to a
frameshift in position 653.
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1317 1317 M -> S (IN REF. 3).
1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
-!- SIMILARITY: TO E.COLI YFAL.
-!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT
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EcoGene; EG11780; ydeK.
InterPro; IPR00437; Prok lipoprot S.
PROSITE; PS00013; PROKRA LIPOPROTEIN; 1.
Hypotheital protein; Membrane; Lipoprotein; Signal;
Complete proteome; Palmitate.
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EMBL, D90793; BAA15190.1; ALT INIT.
EMBL, D90794; BAA15197.1; ALT INIT.
EMBL, X73295; CAA51730.1; ALT FRAME.
MEDLINE=97251357; PubMed=9097039;
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SEQUENCE
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MOM38.";
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Best Local
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1173 GELRNSISGKGIVSATARTDVELDGDNSRFVGQFNID-TGSALSVNEQKNLGDASVINNG 1231
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                                                                                                   282 AIAFKLNDEKGNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATSTTG-----KL 333
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                                                                                                                                                                                                                                                                                                                                                   -----VFALDADNDGVVNY-----GSKLSGK-- 398
                                                                                                                                                                                                                                                                                                                                                                                                            642 LNIGAAHGEAAADAGFITNATKVEFGLGEGVFVFNHTNNSDAGYQVDMLITGDDKDGKVI 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 ----DFALNSQNLVVGEKASLNKLVATIAGE--DKVVDPGSISIKSSNHGIISVVNNYIT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----QYGDPFGANTAAIKEVLPKTGVVAEGGLDVVTTDS--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 878 YTWKGRNYQVNGTGDVLIDVPKPWNDPMANNPLTTLNLLBHDD--SHVGVQLVKAQTVIĞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    632 PENLEGYEVESKNLAVADAKIV---GNKVVV---TGKTPGKV-----DIHLTKNGATAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            681 AT----VEIVQETIAIKSVNFK-PVQTENFVEKKINIGTVLELEKSNL--DDIVKGINLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       734 KETQHKVR----VVKSGAEQ-----GKLYLDRNGDAVF----NAGDVKL---G
                                                                                                                                                                                                                           AVGIK-QGDYKVE------PASAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   702 HDAGHTVFNAGNTYSG-KTLVNDGLLTIASHTADGVTGMGSSEVTIANPGTLDIL---AS
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
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P76856; P76857; P76859;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                               Aiba H., Rabhimoto K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Macobuchi K., Mori H., Motomura K., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takencho K., Takeuchi Y., Mada C., Yamamoto Y., Horiuchi T., Takencho K., Takeuchi Y., Mada C., Yamamoto Y., Horiuchi T., Corresponding to the 28.0-40.1 min region on the linkage map.";
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                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOCHIMIE 73:1361-1374(1991).
-!- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG (AC P25928).
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING I THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT BETWEEN AMINO ACIDS 839 AND 840.
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Mosser I., Glaser P., Danchin A.;
"Multiple IS insertion sequences near the replication terminus
Escherichia coli K-12.";
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22.6%; Pred. No. 0.024;
tive 96; Mismatches 275;
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SURFACE
InterPro; IPR001119; SLH.
Pfam; PF00195; SLH; 2.
PROSITE; PS01072; SLH DOMAIN; 2.
Signal; Cell wall; S-Tayer; Repeat.
SIGNAL
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1116
120
171
231
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57 12
121 17
172 23
1116 AA;
                                                                                                                                            Similarity
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                                                      322 ATANNNGKTTVDGKDSTGTEI-----NGNNGKVIQDGDLDVSGGGHGID----ITGDS 370
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                                        LIVSNIGIITVKNLDIPASAIKNVVFALDADNDGVVNYGS-KLSGKDFALNSONLVVGEK 412
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                                                                                                           ATVDN-----EGESAITNGGTGTQVD--GDQAVVNN-----EGESAITNGGTGTQING
                                                                                                                                                                               TAAIKEVLPKTGVVAEGGLDVV-----TTDSGSIGTKTIG--VTGNDVGEGTVHFQNGN
                                                                                                                                                                                                                            571 GATL-----GSLYV----NVTE-GNVAFKNFELVSKVGQY-----GQSP
                                                                                                                                                                                                                                                                        605 DIKLDLNVS-----ITVEYQLSKYTSDRV--YSDPENLEGYEVESKNLAVADAKIVG
                                                                                                                                  466 GDVTKDVKFKVTTDSRKLVSVKANPDKLQVVQNKTLPVT-----FVTTDQYG-DPFGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ebisu S., Tsuboi A., Takagi H., Naruse Y., Yamagata H., Tsukagoshi
Udaka S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
11-SMAR-2004 (Rel. 43, Last annotation update)
Surface layer protein precursor (Hexagonal wall protein) (HWP)
Brevibacillus choshinensis.
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
11 TaxID=54911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Conserved structures of cell wall protein genes among protein-producing Bacillus brevis strains.";
J. Bacteriol. 172:1312-1320(1990).
-:- SUBCELLUIAR LOCATION (Cell wall. This bacterium is covered layer with hexagonal symmetry.
-:- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
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                                                                                      ASLNKLVATIAGEDKVVDPGSISIKSSNHGIISVVNNYITAEAAGEATLT-
      281 MTVT-----DPESMGIQIDGDKAIVNNEGESTIINGGTGTQINGDD-
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STRAIN=HPD31;
MEDLINE=90170842; PubMed=2307650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 KRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNY-GSKLS-----GKDFA 401
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                                                                                                                                                                                                                                       Gaps
                                                                                                                                                               Conservative 142; Mismatches 347; Indels 362;
                                                                                                                       5.2%; Score 219; DB 1; Length 1116; 19.2%; Pred. No. 0.018;
                                                          31 SLH 3.
123397 MW; 86D583D7AC72546F CRC64;
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  790 VDGSGLGGDHQFGMVKQYGTASKQDTITIVTKDGDSVTEKEYKLDGDADDLKVDQDIRRG 849
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                                                                                                                                                                              904 RVDEVDGNTISLNYADGKTQKYYTKASTAF-IDVYDGLEGIDGVDEGDYIVMIDSADIDG 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stranton J., Walker D., Stenos J., Walker D., "The rickettsia and the spotted fever group."; "The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-layer with hexagonal symmetry (By similarity). SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                        ----LTKETQHKVRVVKSGAEQGKLYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen ) (Saa5) (Saa5) (Yompa Cromp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB)."; int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21442074; PubMed=11557893; Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
                                                                                                                                        RNGDAVFNAGDVKLGDVTVSQTSDSALPNFKADLYDTLT-TKYTDKG-
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                                                                                                                                                                                                                                                          963 TRFDYVLVVSSDDEIRTQHISTKAV-TDFLNKP 994
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16-0CT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        1655 AA
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MEDLINE=20393643; PubMed=10939649;
                                                TVLELEKSN-----LDDIVKGIN-----
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Science 293:2093-2098(2001)
                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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OMPB OR RC1085.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 INTPAGSFNGLFLNTANNLDVTVREDTTLGFITNVVNNANHFNLMLNAGKTLTITGQGIT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 TSAVVTLGGKVAPN-KDLTVKVKNQSFVTKFVYEVKKLAVEKLTFDDDRAGQAIAFKLND 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D----NVNTLNLQANGATITFNGTDGTGRLVLLSKNAAATDFNVTGSLGGNLKGIIEFNT 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 LNGNFTGDASNPGNTAGVITFDANGTLASASADANVAVTNNITAIBASGAGVVQLS-GTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 -RAEAAQFIAL---TDXKYG---KKDNAQAYVTDV------KVSEPTKLTLTGTGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 EKGNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATST----TGKLAVGIKQ----GD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 ASFAGSAMGAAIQQNRTTNAVATTVDGVGFDQTAVPANVAVPLNAVITAG----VNKGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----IISVVNNYITAEAAGEATLTIKVGDV
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G -> S (IN STRAIN INDIAN TICK TYPHUS).
V -> A (IN STRAIN INDIAN TICK TYPHUS).
V -> A (IN STRAIN INDIAN TICK TYPHUS).
N -> D (IN STRAIN INDIAN TICK TYPHUS).
I -> V (IN STRAIN INDIAN TICK TYPHUS).
R -> I (IN STRAIN INDIAN TICK TYPHUS).
R -> GH (IN STRAIN INDIAN TICK TYPHUS).
                                                                                                                                                                                                  Complete proteome.
120 kDa SURFACE-EXPOSED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 217; DB 1; Length 1655;
Pred. No. 0.035;
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E -> D (IN REF. 3).
G -> S (IN REF. 3).
H -> R (IN REF. 3).
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                                             EMBL, AT149110, AAD39533.1; -.
PTR, E97835, B97835.
Interepro, IPR006315, Autotransport.
InterPro, IPR005546, Autotransporter.
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                                                                                                                                                  Pfam; PF03797; Autotransporter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.2%;
EMBL; AF123721; AAF34124.1;
EMBL; AF123726; AAF34129.1;
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1177
1492
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CHAIN 1 1334
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572 TIKLTSTQNNIVV-DFDLAIATDQTGVVDASSLTNAQTLTINGKIG-----TVGANNKTL 625
                                                                                              683
                                                                                                                                                                                                                                                                               587 OETIAIKSVNF----KPVQTENFVEK-KINIGTVLELEKSNLDDIVKGINL--TKETQHK
                                                                                                                                                                                                684 NNTTLATGTVLGSATNPLAEINFGSKGAANVDTVL-----NVGKGVNLYATNITTTD
                                                                                                                                                                                                                                                740 VRVVK------SGAEQGKLY----LDRN-----GDAVFNAGDVKLGDVTVS
                                                                                                 626 GOFNIGSSKTVLSDGDVAINELVIGNN--GAVQFAHNTYLITRTANAAGQGKIIFNPVVN
                                                  EGYEVESKNLAVADAKI VGNKVVVTGKTPGKVD - - - - - I HLTKNGATAGKATVEIV - -
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TSUDDIA., Uchini R., Engelhardt H., Hattori H., Shimizu S.,
Tsukagoshi N., Udaka S.;
Tsukagoshi N., Udaka S.;
Tsukagoshi N., Udaka S.;
Tsukagoshi N., Udaka S.;
Tsukagoshi N., Udaka S.;

Tsukagoshi N., Udaka S.;

Tsukagoshi N., Udaka S.;

Protein synthesized by Bacillus subtilis harboring the surface layer protein synthesized by Bacillus subtilis harboring the surface layer protein error from Bacillus brevis 47.";

-: FUNCTION: The middle wall protein binds to peptidoglycan and to the outer cell wall protein.

-: SUBJUNIT: THE MIDDIA CELL WALL LAYER IS CONFOSED OF SUBJUNITS OF THE MIDDIA CELL WALL THESE PROTEINS FORM A HEXAGONAL
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Tsubol A., Uchihi R., Adachi T., Sasaki T., Hayakawa S., Yamagata H.
Tsuboshi N., Udaka S.;
"Characterization of the genes for the hexagonally arranged surface
layer proteins in protein-producing Bacillus brevis 47: complete
nucleotide sequence of the middle wall protein gene.";
                                                                                                                                                                                                                                                                                                                                                                            990 ANSTLOIGGNYTADFVASA-----DGTGIVEFV-NTGPITVTLNKQAAPVNAL 836
                                                                                                                                                                                                                                                                                                                                               776 QTSDSAL-PNFKADLYDTLTTKYTDKGTLVFKVLKDKDVITSEIGSQAVHVNVL 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDITION 19, Uchihi R., Tabara R., Takahashi Y., Hashiba H., Sasaki Tsuboi A., Uchihi R., Tabara R., Takahashi Y., Hashiba H., Sasaki Yamagata H., Tsukagoshi N., Udaka S., "Characterization of the genes coding for two major cell wall Characterization of the genes coding for two major cell wall protein from protein-producing Bacillus brevis 47: complete nucleotide sequence of the outer wall protein gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Middle cell wall protein precursor (MWP).
Bacillus brevis (Brevisbacillus brevis).
Bacteria; Firmicutes; Bacillales; Paenibacillas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamagata H., Adachi T., Tauboi A., Takao M., Sasaki T., Tsukagoshi N., Udaka S.; Tsukagoshi N., Udaka S.; Cloning and characterization of the S' region of the cell protein gene operon in Bacillus brevis 47."; J. Bacteriol. 169:1239-1245(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 06, Created)
(Rel. 12, Last seq
(Rel. 43, Last ann
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AC SLOW_BACBR

AC SLOW_BACBR

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DT O1-JAN-1988

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DT O1-JAN-1988

DT O1-JAN-1988

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                                 WALL LAYERS.
SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
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ARRAY WITH A LATTICE CONSTANT OF 14.5 NM IN THE MIDDLE
                                                                                layer with hexagonal symmetry. SIMILARITY: Contains 3 S-layer homology (SLH) domains.
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117146 MW; DB4213188D9D5E4F CRC64;
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5.0%; Score 211; DB
Best Local Similarity 19.9%; Pred. No. 0.036
Matches 193; Conservative 138; Mismatches
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PROSITE; PS01072; SLH DOMAIN; 2.
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EMBL, M14238, AAA22372.1; -.
EMBL, M19115, AAA22760.1; -.
EMBL, M31828; AAA22619.1; -.
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Similarity
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                                                                                                        YQLSKYTSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVVTGKTPGKVD-IHLTKNGA
                               VOKVVSRNNNDYRLTIGDKTYRVYEGATFSDDGNKDVQDIDKDHWDLVDSLDDETVKLYL
                                                          NVTEGNVAF------TVE-----TVE-----
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                                                                                 DAS-GRVRHIETKDAIDDRKQKAIVTRSATFNTSKDT-WDFRVLTQKGKEITVSLEAKNI
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15-UUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide)
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Rickettsia typhi and Rickettsia
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Hackstradt T., Messer R., Cieplak W., Peacock M.G.;
Hackstradt T., Messer R., Cieplak W., Peacock M.G.;
Evidence for proteolytic cleavage of the 120-kilodalton outer membrane protein of rickettaiae: identification of an avirulent mutant deficient in processing.";
Infect. Immun. 60:159-165(1992).
-: FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=785;
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              LDVVTTDSGSIGTKTIGVTGNDVGEGTVHFQNGNGATLG-
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MEDLINE=94040787; PubMed=8224886;
Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
"Cloning and sequence analysis of the gene en
surface layer protein of Rickettsia typhi.";
Gene 133:129-133(1993).
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MEDLINE=92114896; PubMed=1370573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 VQLSGIHGARLRLGNAGSIFKLADGİVINGPVNQNPLVNNNALAAGSIQLDGSAIITGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 ASFASMLVSAYNLKDKVNGELVTTFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGFSGVAMGAVMQYNRTINAAATT----VDGAGFDQTGAGVNLPVAINSVITANSNNAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTLG--GKVAPNK----DLT---VKVKNQSFVTKFVYEVKKLAVEKLTFDDDRAGQAIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVVAEGGLDVVTTDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----RAEAAQFIALTDKKYGKKDNAQAYVTDV------KVSEPTKLTLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 IQSAN--AGGQVTFEHLVDVGLGGKTNFKTADSKVIITENASFGSTDFGNLAVQIVVPNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION. FUNCTION: THE 32 KDB BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR. SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1645;
                                                                                                                                                                                                                                                                                                                                                                                                                                 layer with hexagonal symmetry.
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.9%; Score 207.5; DB 1;
ilarity 20.6%; Pred. No. 0.091;
Conservative 130; Mismatches 346;
                                                                                                                                                                                                                                                                                                                                                                 PIR; JN0896; JN0896.
InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
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             APKNFELVSKVGQYGQSPDTKLDLNVSTTVEYQLSKYTSDRVYSDPENLEGYEVESKNLA 646
                                         637
                                                                  694
                                                                                              693
                                                                                                                       740
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                                                                                                                                                                            ----RVVKS--GAEQG----KLYLDRN-----GDAVFNAGDVKLGDVTVSQTSDSALPN 784
                                                                                                                                                                                              - LVDFDLDVTTDQTGVVDASSLTNNQTLTINGSIG-----TIGANTKTLGRFNVGSSKTI
                                                                   647 VADAKIVGNKVVVTGKTPGKVDIHLTK-----NGATAGKATV---EIVQETIAIKS
                                                                                                                                                   TNLGSAESPLSNIHFATKAANGDSILH-----IGKGVNLYANNITTTDANVGSLHFR
                                                                                              LNAGDVAINELVM--ENDGSV--HLTHNTYLITKTINAANQGKIIVAADPINTDTALADG
                                                                                                                       VNF----TKPVQTENFVEKKINIGTVLELEKSNLDDIVKGINL----TKETQHKV-----
                                                                                                                                                                                                                                   F--KADLYDTLTTKYTDKGTLV------FKVLKD------KDVITSEIGSQAVH 824
                                                                                                                                                                                                                                                            HIESADNIGTLEFVNIDPITVTLNKQGAYFGVLKQVMVSGPGNIAFNEIGNGVAH 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Mada C., Yanamoto Y., Horiuchi T., Takeda J., Takemoto K., Mada C., Yanamoto Y., Horiuchi T., Mada C., Yanamoto Y., Horiuchi T., Daya Sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SIMILARITY: Contains 13 Big-1 domains.
                                                                                                                                                                                                                                                                                                                                           75437; P94750; 28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last sequence update)
41, Ppothetical protein yeeJ.
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                                                                                                                                                                                                                                                                                                                                    2358
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EMBL; D90837; BAA15800.1; -.
EMBL; D90836; BAA15799.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAINEH12;
MEDLINE=97251358; PubMed=9097040;
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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EcoGene; EG13378; yeeJ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1521 GKAKVTIKGTKAGAHTVTASMTGGKSEQLVVNPIADTLTAQVNLNVTEDNFIANNVGMTR 1580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 ---KINDEKGNADVEYINLANHDVKFVANNLDGSPANIF-----EGGEA-TSTTGKLAV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GIKQGDYKVEVQVTKRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYG 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 -----GKWEPNKSVSRAEAAQFIALIDKKYGKKDNAQAYVIDVKVSEPTKLTLTG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1581 LQATVTDGNGNP-----LANEAVTFTL-----PADVSASFTLGQGGSAITDINGKAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1236 TVHFIGDTAAAKIIELAPVPDSIIAGTP--QNSSGSVITATV----VDNNGFPVKGVTVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1290 FTSNAATAEMTNGGQAVTNEQGKATVTYTNTRSSIESGARPDTVEASLENGS--STLSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 08 NNAIYTTNHDGNFYASFTATKAGVYQLTATLB----NGDSMQQTVTYVPNVANAEITLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393 SKLSGKDFALNSQ-----NLVVGEKASLNKLVATIAGEDKVVDPGSISIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 SNHGIISVVNNYITAEAAGEATLTIKVGD-----VTKDVKFKVTTDSRKLVSVKANPDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 IWSSKYIAAVEKAG--VVKGDGKENF------YPEGKIDRASFASMLVSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 YN------LKDKVN-GELVTTFEDLLDHWGEEKANILINLGISVGTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 LTVKV------KNOSFVTKFVYEVKKLAVEKLTFDDDRAGQAIAF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.9%; Score 207.5; DB 1; Length 2358;
llarity 20.2%; Pred. No. 0.14;
Conservative 126; Mismatches 390; Indels 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 S -> G (IN REF. 2).
AA; 248599 MW; 232249750BF631ED CRC64;
                                                                                                                                                                                                        proteome
InterPro; IPR003344; Big_1.
InterPro; IPR003555; Intimin.
InterPro; IPR008964; Invasin_intimin.
InterPro; IPR008964; Invasin_intimin.
InterPro; IPR000601; PKD.
FRINTS; PR01369; Big_1; I3.
FRINTS; PR01369; INTIMIN.
SWART; SW00534; BID 1; I3.
SWART; SW00534; BID 1; I3.
SWART; SW00599; PKD; 6.
Hypothetical_protein; Repeat; Complete;
                                                                                                                                                                                                      Complete
                                                                                                                                                                                                                                                                                   BIG-1 4.
BIG-1 5.
BIG-1 6.
BIG-1 7.
BIG-1 9.
BIG-1 10.
BIG-1 110.
BIG-1 111.
BIG-1 111.
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11661
11953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

C STRAIN-0157:H7 / RIMD 0509952;

MEDINIE-2115631; Pubmed=11258796;

MEDINIE-2115631; Pubmed=11258796;

Hayabhi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayabhi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T.,

A Han C.-G., Ohrebubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Xasunaga T.,

Ruhara S., Shiba T., Hattori M., Shinagawa H.;

Ruhara S., Shiba T., Hattori M., Shinagawa H.;

T. "Complete genome sequence of enterchemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001)

- I- SIMILARITY: Contains 16 Big-I domains.

- I- SIMILARITY: Belongs to the intimin/invasin family.

- I- SIMILARITY: Ref.2 sequence differs from that shown due to a frameshift in position 1315.
                                                                                                                                                                                                                                                      1776 MVAQD--VAVKAHVNDQFGNPVAHQPVTFSAEPSSQMIISQN----TVSTNTQGVAEVT 1828
                                                       1889 IPVEGOVINFS---VTPEGATLSGGKVRINSSGQAPVVLISNKVGTYTVTASFHNGVTIO 1945
                                 VTGNDVGEGTVHFQNGNGATLGSLYVNVTEGNVAFKNFELVSKVGQYGQSPDTKLDLNVS 613
                                                                                                                                                                671 -----LTKNGATAGKATVEIVQETIAIKSVNFKPVQ------TENFVEKKINIGTVLBL 718
                                                                                                                                                                                         1946 TOTTVKVTGNSSTAHVASFIADPSTIAATNTDLSTLKATVEDGSGNLIEGL----TVYFA
                                                                                                  614 TIVEYQLSKYISDRVYSDPENLEGYEVESKNLAVADAKIVGNKV---VVTGKTPGKVDIH
                                                                                                                                                                                                                                  719 EKSNLDDIVKGINLTKETQHKVRVVKSGAEQGKLYLDRNGDAVFNAGDVKLGDVTV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-6157:H7 / EDL933 / ATCC 700927;

STRAIN-6157:H7 / EDL933 / ATCC 700927;

STRAIN-6157:H7 / EDL933 / ATCC 700927;

PEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rosefai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

Welch R.A., Blattner F.R.;

Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                     YEEJ ECO57 STANDARD; PRT; 2660 AA. 08x807; 08x209; 08x200; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein yeeJ. 23.135 OR ECS2775/ECS2776. Escherichia coli 0157:H7.
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NCBI_TaxID=83334;
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Best Local Similarity 20.3%; Pred. No. 0.17;
Matches 197; Conservative 134; Mismatches 387;
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EMBL; AP002559; BAB36199.1; ALT_FRAME.
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InterPro; IRR008964; Invasin_intimin.
InterPro; IRR008964; Interpro; IRR008964; InterPro; IRR008969; RED; 16.
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SMART; SM00644; BID 1; 16.
SMART; SM00699; PRD; 8.
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497 ONKTLPVTFVTTDOXGDPFGANTAAIKEVLPKTGVVAEGGLDVVTTDSGSIGTKTIGVTG 556 	NDVGEGTVHFONGNGATLGSLYVNVTEGNVAFKNYELVSKVGOYGQSPDTKLDLAVSTTV 616 	EYQLSKYTSDRVYSDPENLEGYEVESKULAVADAKIVGNKVVVTGKTPGKVDIHLIKNGA 676 : :	677 TAGKATVEIVQETIAIKSVNFKPVQTENFVEKKINIGTVLELEKSNLDDIVKG 729 	INLTKETQHKVRVVKSGAEQGKLYLDRNG	DVIVSQTSDSALPNFKADLYDTLTTKYTDKGTLVFKVLKDKDVITS 816 	817 BIGSQAUHUNU 827 	
ONKTLPVT : : QDvavk	NDVGEGTV NGSYMV	EYQLSKYT ::: EGQVINFS	TAGKATVE T	INLTKETQ : : LTV		EIGSQAVHVNV 827 : GTNAPYVQV 241	
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Search completed: April 7, 2004, 17:33:32 Job time : 24 secs

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GenCore version (c) 1993 - 2004
            Copyright
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protein search, using sw model OM protein

Run on:

April 7, 2004, 17:26:39; Search time 24 Seconds (without alignments) 3338.648 Million cell updates/sec

US-09-844-281-1 4202 score: Sequence: Title: Perfect

1 AGKSFPDVPAGHWAEGSINY.....ITSEIGSQAVHVNVLNNPNL

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1	JC4930	S-layer

S-layer protein precursor - Bacillus licheniformis
C;Species: Bacillus licheniformis
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C;Species: Bacillus licheniformis
C;Accession: J04930
R;Zhu, X.; McVeigh, R.R.; Malathi, P.; Ghosh, B.K.
Gene-173, 189-194, 1996
A;Title: The complete nucleotide sequence of the Bacillus licheniformis NM105 S-layer-e: A;Title: The complete nucleotide sequence of the Bacillus licheniformis NM105 S-layer-e: A;Title: The complete nucleotide sequence of the Bacillus licheniformis NM105 S-layer-e: A;Status: preliminary
A;Reference number: J04930; MUID:97082965; PMID:8964497
A;Status: preliminary
A;Molecule type: DNA
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7; Gaps 23; Query Match 67.4%; Score 2833.5; DB 2; Length 874; Best Local Similarity 67.3%; Pred. No. 3.1e-125; Matches 569; Conservative 98; Mismatches 156; Indels 23;

9 30 AGKSFPDVPAGHWAEDSINYLVDKGAIVGKPDGTYGPTESIDRASAAVIFTKILNIPVDE.89 1 AGKSPPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDE qq

61 NAQPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKV 120 149 90 NAQPSFRDARNIWSSRYIAAVERAGVVKGDGKDNFYPEGKIDRASFASMLVGAYNIKEKV Š 쉱

180 209 121 NGELVTTFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGK ò 엄

241 VAPNKDLTVKVKNOSFVTKFVYEVKKLAVEKLIFDDDRAGQAIAFKLNDEKGNADVEYLN 300 à

329 a

389 301 LANHDVKFVANNLDGSPANIFEGGEATSTTGKLAVGIKQGDYKVEVQVTKRGGLIVSNTG 360 à g

Db 149 NGTPATKFKDLETLNWGKEKANILVELGISVGTGDOWEPKKTVTKAEAAGFIAKTDKGFG 208 Qy 180KKUNAQAYTDVKVSEPTKLITGTGLDKLSADDVILEGDKAVAIEA 226 Db 209 TEAAKVESAKAVTTGKVEVKESKAVEKLIKEDIKYTNKANNDKVLVKEVIL 259 Qy 227 STDGTSAVTTGGKVAPKDLTVKVKNGSFYTKFVTSHKANNDKVLVKEVTL 259 Qy 227 STDGTSAVTTGGKVAPKDLTVKVKNGSFYTKFVTSHKANNDKVLVKEVTL 259 Db 260 SEDKKASATTELYSUNARKOTYTVVDNKVGKTEVAPGSLEAKTIENDDRAGQA 282 B1 1 LAFKLNDEKGNADVEYLMIANHDVKFVANNILDGSPANIFEGGEATSTTGKLAVGTKGDS 342 Db 317 LQFTVKDENGTEVVSPEGIEFVTPAFEKINAKGEITLAKGTS 358 Qy 343 KVEVQYTKGGGLTVSNTGITTYKNLDTPASAIKNVVFALDADNDGVVNYGSKLGSGKDPAL 402 Db 318 TVKAVYKKGGKVVAESKEVKVSAEGAAVASISNMTVAEQNKADFTRNDFKQ 410 Qy 461 LTIKVGDVTKDOFKNYTTGAEDKVVDRATGKVTVLSAGKAP 466 Qy 462 LTIKVGDVTKDOFKNYTTGAEDKVVDRATGKVTVLSAGKAP 466 Qy 463 NSQNLVVGSKALVSKTVEIEAFAGKANKEIKLEKTNVALGTTGVTGVTDVTTDQYGG 513 461 LTIKVGDVTKDVKKV-TTDSSKLVSVKANPDKLQVVQNKTLPVTTDQYGG 513 MY TYTYCDSKGKELVSKTVEIEAFAGKANKEIKLEKTNVALGTTGVTGVTDQYGG 510 DD 527 BFTAPVTVKVLDKOGKELKGKKEAKKTNYRELYLNAAGQEAGNTTVVLTAKSGE 580 Qy 671 GATLGGLYNVPDEGNYRKRGFEV	Db 620 NAMTYSVLPUDATIALIXYMERATELATTHNEGREWUATDAQVTVQNANSTITVGQALKA 679 Qy 679 GKA-TVELVOETIALKSVNEKRVQTENEVEKKINIGTVLELEKGNLDDIVKGINL 732 Db 680 GETYKVTVULDGKLITHSFKVVQTENEVEKKINIGTVLELEKGNLDDIVKGINL 729 RESULT 3 A33856-18-9 SALINUS SPLANTUS. G.Specides: Bacillus spharaticus G.Specides: Bacillus spharaticus G.Specides: Bacillus spharaticus G.Specides: Bacillus spharaticus G.Specides: Bacillus spharaticus G.Specides: Bacillus spharaticus G.Specides: Bacillus spharaticus G.Specides: Bacillus spharaticus G.Specides: Bacillus spharaticus G.Specides: Bacillus spharaticus G.Specides: Bacillus spharaticus A.Stillis (1989) A.Title: Cloning and sequencing of the gene encoding a 125-kilodalton surface-layer pro A.Stelenene unmber: A33856; MUID:89327128; PMID:2666389 A.Stillis (2004) A.Stillis (2004) A.Stelenene unmber: A33856; MUID:89327128; PMID:2666389 A.Stelenenes and San M28361; NID:9341911; PIDN:AASO256.1; PID:9556012 A.Stose-references and San M28361; NID:9341911; PIDN:AASO256.1; PID:9556012 A.Stose-references and San M28361; NID:9341911; PIDN:AASO256.1; PID:9556012 A.Stose-references and San M28361; NID:9341911; PIDN:AASO256.1; PID:9556012 A.Stose-references and San M28361; NID:9341911; PIDN:AASO256.1; PID:9556012 A.Stose-references and M242; Pace A No. 1.2e-08; Matches 236; Conservative 123; Mismatches 307; Indels 310; Gaps 55; A. Matches 236; Conservative 123; Mismatches 307; Indels 310; Gaps 55; A. MACCHARAVOSLVADAGVIQGDANGNENPERATERNALELEAEGDVNFEWUXAD 99 A. TAKRAVOSLVADAGVIQGDANGNENPERATERNALELTHURDELTTFED- Db 100 AWYYDAIAATVENGTERDAAATTFTNALELEAEGDVNFEWUXAD 156 Db 100 AWYYDAIAATVENGTERDAAATTFTNALELEAEGDSODL-SEPAD 156
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A; Molecule type: DNA A; Residues: 1-762 < PET> A; Residues: 1-762 < PET> A; Cross-references: GB:MJ1069; NID:g141844; PIDN:AAA21930.1; PID:g141845 C; Superfamily: S-layer repeat homology < GLR1> F; 32-85/Domain: S-layer repeat homology < SLR1> F; 96-150/Domain: S-layer repeat homology < SLR2>	Query Match 6.3%; Score 265.5; DB 2; Length 762; Best Local Similarity 22.7%; Pred. No. 4.6e-05; Matches 193; Conservative 116; Mismatches 347; Indels 193; Gaps 44;	47 AVIFTKILNLPVDENAQPS :- : 5 ALVFSAMAVGFAATTE	Qy 104 ASFASMLVSAYNLKDKVNGELVTTFEDL-LDHWGEEKANILINLGISVGTG-GKWEP 158	Qy 159 NKSVSRABAAQFIALTDKKYGKKDNAQAYVTDVKVSEPTKITLTGTGLDKLSAD 212	Qy 213 DVTLEGDKAVAIEASTDGTSAVVTLGGKVAPNKDLTVKVKNGQSFVTKFVYEVKKLAVEK- 271	272LTFDDDRAGQAIAFKLNDEKGNADVSYLNLAN	Db 234 KVAVLDKDGKLTTINAGLVDFSEYLGKAVIVISBKFGJFVIVAKEGJAJVVS 201 OV 328 STTGKLAVGIKQGDYKVEVQVTKRGGLTVSNTGIITVKNLDTFAS 372	265 FTEGODSVGTTVYKNDDNKTAIKVDDNAYVLYNGYLTKVSKVTVKEGAEVTIN 33	QY 373 AIKNVVFALDADNDGVVNYGSKLSGKDFALNSQNLVVGEKASLNKLVATIAGEDKVVDPG 432 QY :::::	AEAAGEATLTIKVGDVTKDVK	389 IK	YTVADNNVWNQLEPGKKVTVILNKDNVIVGISSTTTTTAVNYAIFKEKSDFFTAWFAKVK	QY 524 EVLPKTGVVAEGGLDVVTTDSGSIGTKTIGVTGNDVGEGTVHFQNCNGAT 573	574 LGSLYVN-	2 FSSASYKADAKVLTEGSTTYYITDNTVLL	YSDPENLEGYEVESKNLAVADAKI VGNKVVVICKIFCKVULINILAMAKIAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	682 TVEIVQETIAIKSVNPKPVQTENFVEKKINIGTVLELEKSNLDDIVKGINLTKETQHK	652	OY 740 VRVVKSGAEQGKLYLDRNGDAVFNAGDVK-LGDVTVSQTSDSALPNFKADLYDTLTTKYT 798	Db 708 LRITDT-TNKGYL-LDPNFIVVDINGNLKGLSDITKDTGVNLYT 749	Qy 799 DKGTLVFKV 807	DD 750 NDVGKVFVI 758	RESULT 5
Qy 131 -LLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGKKDNAQ 185 157 STVKPWAKSYLEIAVANGVIKGSEANGKTNLNPNAPITRQDFAVVFSRT 205 Qy 186 AYVTDVKVSEPTKLTLTGTGLDKLSADDVTLGGDKAVAIEAST	Db 206KALDEN 242 Oy 240 KVAPNKDLTVKYKNQSFVTKFVYEV	243 ALEPÜNKETEVTFKIKUVEYKAKVTYVVTTATAVKSVSATNLKEVVVËFDGTVDKETAEDA 283 IAFKLNDEKGNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATSTTGKLAVG :	303 ANYALKSGKTIKSVSLAADNKTATVTLTDKLNNNKADAIS 3 337 IKQGDYKVEVQVTKRGGLTVSNTGIITVK-NLDTPASAIKNVVF 3	Db 343 ISNVKAGDKEINVKAVDFTTAVDNKIPEVTEVKSLGTKAVKVTLSEPVENLSSTNF 397 Qy 380 ALDADNDGVV-NYGSKLSG-KDFALNSQNLVV 409	DD 398 TLDGKAYFGNVVMGÅGNKTVILTPYSSSALSVGDHKLTVSGAKDFAGFVSLNSTHBFKVV 457 QY 410 GEKASLNKLVATIAGEDKVVDPGSISIKSSNHGIISVV 447	DD 458 EDKEAPTVTEATATLETVTLTFS-EDIDMDTVKASNVYWKSGDSKKEASEFERIAD 512 OV 448 NNYTTAEAAGEATL-TIKVGDVTKDVKFKVTTDSRKLVSVKANPDKLQVVQ 497	513	Oy 498 NKTLEVTTDQXGDFFGANTAAIKEVLEKTGVVAEGGLDVVTTDSGSIGTKTIGVTGN 557	5/3 BRITAVIFSKLYDGESALKLIGNIIVALADA - VANATELYSKYGOYGOSPDIKLDLAVSTI 558 DVGEGTVHFQNGARLGSLYVANYTEGNVAFKANFELVSKVGOYGOSPDIKLDLAVSTI : : :	615KDSKSVIIDLYSKVSVGENTITIKÄVKKDATK	ASLADY	670HITKNGATAGKATVEIVQETIAIKSV-NFKPVQTENFVEK7	TLVKI TIGTVLEL	LAKIDK	OY 757 NGDAVENAGDVKLGDVTVSQTSDSALFN-FKADLYDTLTTKYTDKGTLVFKVLKDK 811	812	: : : : : : : :	и напод	nacour : Barriage protein precursor - Acetodenium kivui	Species: Acetogenium kivui Date: 15-Jun-1990 #Bequence revision 15-Jun-1990 #text_change 08-Oct-1999	; Accession: A34355 Lottspeich, F.; Baumeister, W.	J. Bacteriol. 171, 6307-6315, 1989 A:Title: S-layer protein gene of Acetogenium kivui: cloning and expression in Escherichi A:Reference number: A34355; MUID:90036724; PMID:2681162	A;Accession: A34355

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                                                                                                                                                                                                                                                                                                                 802 DSAATPNTNEKLOALKSVLSGIVSSDTSVIGSVSNVDNLKDDASISGLAVKKAGTVTLTL 861
                                                                                                                                                                                                                                                                                                                                                                                                                       766 ----DVKLGDVTVSQTSDSALPN----FKADLYDTLT----TKY--TDK---GTLVFKVL 808
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     ---GTVLELEKSNLDDIVKGIN---- 731
                                                                                                     744 GİVILGIVDVEVIDİTLKATVVIKKADLIELDAADNĞDALAKLLANLD--IKDQMCNPMV 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 862 VFNEDSKIAPIAITVKAPAATQDGVTVTGLDLVPGVTGVGKTKFTATDKIKSGHKLYYAV 921
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                                                                                                                                                                                                                 732 ---LTKETQHKVRVVK------SGAEQGKLYLDRNGDAVFNAG----
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Matches 193; Conservative 109; Mismatches 291; Indels 311;
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     688 ETIAIKSVNFKPVQT---ENFVEKKINI---
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Cispecies: M.; Egelseer, E.M.; Mattanovich, D.; Sleytr, U.B.; Sara, M.
Submitted to the EMBL Data Library, April 1999
A; Description: Nucleotide sequence of the coding region of sbsC, the S-layer gene from 18, Reference number: 21823
A; Reference number: 21823
A; Reference number: 21823
A; Reference number: 21823
A; Residues: 1-1099
A; Residues: 1-1099
A; Residues: 1-1099
A; Construction of the Coding region of SbsC, the S-layer gene from 18, Status: preliminary, translated from GB/EMBL/DDBJ
A; Residues: 1-1099
A; Construction of SbsC, the S-layer gene from 18, Status of SbsC, the S-layer gene from 18, Status of SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC, SbsC
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6.1%; Score 255.5; DB 2; Length 1099;
Best Local Similarity 22.0%; Pred. No. 0.00023;
Matches 214; Conservative 125; Mismatches 330; Indels 303; Gaps 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 FYPEG-----KIDRASFASML-----VSAYNLK-------117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 DTAGKEFETSINEFTY--NKPVPASITFNFNKLPEDSAVDL-----TKYVT----V 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 KFVANN-----LDGSPANIFEGGEATSTTGKLAVGIKQGDYKVEVQVTKRGGLIVSNT 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 DKVNGE----LVTTF----IN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 DRVYĞQSTRELLRSTFKADAQALRDRLIYDITVAMKARBAQDAVKAGNLDKAKAALDQVN 231
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956 SNGTVMSNGLLNIIAKQGNITNKN--LIASRQQLNLTAVADNITNDSNISNKIAVLHSLG 1013
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R;Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A;Title: Raemophilus ducrey! secretes a filamentous hemagglutinin-like protein.
A;Feference number: 220984; MUID:9903026; PMID:9811662
A;Accession: T31105
A;Accession: T31105
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-4919 <WAR>
A;Residues: 1-4919 <WAR>
A;Cobestion: 1-4919 <WAR>
A;Cobestion: 1-4919 <WAR>
A;Cobestion: BMBL:AF057696; NID:g3929021; PID:g3929023; PIDN:AAC79761.1
A;Genetics: 1-59A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 ------AGVNHQGVIFAEDDINILTDDGNSRINKVYADYVRVVGKDIELANNG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLVTTFEDLLDHWGEEKAN----ILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKY 178
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5.7%; Score 240.5; DB 2; Length 4919;
Best Local Similarity 20.4%; Pred. No. 0.0099;
Matches 206; Conservative 147; Mismatches 353; Indels 305;
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R;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehle R;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehle J. Bacteriol. 181, 6509-6515, 1999
A;Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbor A;Reference number: A59091; MUID:99445483; PMID:10515943
A;Accession: B59102
A;Status: pre-liminary
A;Molecule type: DNA
A;Kesidues: 1-652 < OXIX-A;Access: GB:AF065404; NID:94894216; PIDN:AAD32394.1; PID:94894306
A;Experimental source: strain Sterne
A;Note: similar to hypothetical protein; PFB0765w (980 aa); Plasmodium falciparum (AE00)
                                                                                                                                                                                 1102 VORI------GKIYAGR--DLTFNKSNAGGKSEIINRGTINVKNKLSYDSDVSFENN 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 AQPSFKDAKOIWSSKY---IAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 AQNPYRDV-NKSSTMFLDEILTLTKMGIFSGDEKGNFRPKSPISRAEMTQVIKNAFNI-- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 FEDLVNKEKQLDELNKRRDVINQKIDE------FDKLNSQRKDLERMLEELNQKLS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 AIEASTDGTSAVVTLGGKVAPNKDLTVKV-KNOSFVTKFVYEVKKLAVEKLTFDDDRAGQ 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 QLKQQ---SPQLQDLKNKLKESQSRLLELNKKDSNRLEINSEIKKL-------NDRKAE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 AIAF------KINDEKGNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 TTGKLAVGIKQGDYKVEVQVTKRGGLTVSNTGII------TVKNLDTPASAIKN--- 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 KYNGELVTTFEDLL-DHWGEEKANILINLGISVGTG-GKWEPNKSVSRAEAAQFI---- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 ---ALTDKKYGKKDNAQAYVTDVKVSEPTKLTLTGTGLDKLSADDVTLE-----GDKAV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 KKAELNTKLVE-LFKVQEALNKKSGQYLYYINKLDNELRELADKYKNSDNKISRLKNHIG 421
678 AGKATVEIVQETIAIKSVNFKPVQTENFVEKKINI-GTVLELEKSNLDDIVKGINLTKET 736
                                                                                                                        737 QHKVRVVKSGAEQGKLYLDRNGDAVFNAGD-----VKLGDVTV----SQTSDSALPN- 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VVFALDADNDGVVNYGSKLSGKDFALNSQNLVVGBKASLNKLVATIAGBDK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 BYNKQLEKIBNELEBCNKKIDNTKKQLABFDKSNKKQQBLESBLVQLNKKIDBLGKRHK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,Species: Bacillus anthracis
,Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SFPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRAS-AAVIF-TKILNLPVDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 PVVGK--HNFRDVAKDYWANDAISALQSNQLVSGTGNGLFEPYKSVTREEYAQFIFNVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein pXO1-90 - Bacillus anthracis virulence plasmid pXO1
                                                                                                                                                                                                                                                                                     1151 MQSQKVDLY-----TKIFEAKSDIELTFKTNGTHPVYLNFKSNNN 1190
                                                                                                                                                                                                                                             785 ---FKADLYDTLTTKYTDKGTLVFKVLKDKDVITSEIGSQAVHVNVLNNPN 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%; Score 239.5; DB 2; Length 652; 23.8%; Pred. No. 0.00061; tive 80; Mismatches 188; Indels 97
                                              1058 EGQASYKLYQ---ASNGGHFGNDGSSGYSEGDLNIKGKFADLD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 23.83
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: pXO1-90
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Cigocies: Listeria innocua
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Cidocesion: AC1533
Ridiaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
i, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
bominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Reference number: Aslo77; MUD:21537279; PMID:11679669
A;Accession: AC1533
A;Accession: AC1533
A;Actession: AC1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47;
                                                                                                                                                                                                                       977 VAIDLGKUTAIDKVUVSSTKISDKSN-DASIKADLVSITNALSGD-QIVLKGATSIKDRG 1034
                                                                                                                                                                                                                                                                                                                                                                   1035 DLSGEANLLAALGKLG-----ESKDGTLA------DTTAEVFTYKGNTYVVDAAGDAAF 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule_type: DNA_A;Residues: 1-1386 <GLA>A;Residues: 1-1386 <GLA>A;Residues: 1-1386 <GLA>A;Crosesreferences: GB:AL592022; PIDN:CAC96035.1; PID:g16413254; GSPDB:GN00178A;Experimental source: strain Clipl1262C;Genetics:
                                                                                                                                                700 VQTE---NFVEKKINIGTVLELEKSNLDDIVKG--INLTKETQHKVRVVKSGAEQGKLYL 754
                                                                                                                                                                                                                                                                                             755 DRNGDAVFNAGDVKLGDVTVSQTSDSALPNFKADLYDTLTTKYTDKG-TLVFKVLKDKDV 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    729
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   558 VVICKIPGK--VDIHLIKNGAIAG--KAIVEIV-------QEIIAIKSVNFKP 699
                                                                          918 TVTPDTAAADLKTIDLSGLSATGGTLASTITLVAANTAITSVKGSLGADTITVVSAN-KA 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                surface protein (LPXTG motif) [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 -YIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKD-KVNGELVTT---FEDL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 LDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGKKDNAQAYVTDV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 730 TVKANQA----TLEAKDSALYVGDTWNSKONFISATÖKDĞTPVDFKDIKVEGTVÖTTKA 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 ----VEYL--NLANH---DVKFVANNLDGSPANIFEGGE------ATSTTGKLAVGI 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 KQGDYKVE--VQVTKRGGLTVSNTGIITVKNLDTPASAIKNVVFALDAD-----NDGVV 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       844 K--DIKVBGTVDTTKAG------TNKVTYTYTAANQSKEVTITVKADQATLEAKDSII 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 KVSEPTKLTLTGTGLDKLSAD - DVTLEGDKAVAIBASTDGTSAVVTLGGKVAPNKDLTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 KVK-NQSFVTKFVYEVKKLAV------EKLTFDDDRAGQAIAFKLNDEKGNAD----
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5.6%; Score 233.5; DB 2; Length 1386;
Best Local Similarity 21.9%; Pred. No. 0.0034;
Matches 197; Conservative 121; Mismatches 339; Indels 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1083 ANNDI 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                              814 ITSEI 818
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                                                                                         Claccesion: AS6143

S. Poworkin, J.; Tummuru, M.K.R.; Blaser, M.J.
J. Bacteriol. 177, 1734-1741, 1995

A;Title: A lipopolysaccharide-binding domain of the Campylobacter fetus S-layer protein
A;Title: A lipopolysaccharide-binding domain of the Campylobacter fetus S-layer protein
A;Reference number: AS6143; MUID:95204338; PMID:7896695
A;Reference number: AS6143; MUID:95204338; PMID:7896695
A;Status: preliminary
A;Molecus: DNA
A;Residues: 1-1109
A;Cross-references: GB:S76860; NID:9913763; PIDN:AAB33871.1; PID:9913764
A;Cross-references: GB:S76860; NID:9913763; PIDN:AAB33871.1; PID:9913764
A;Gene: sapA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVVKGDGKENFYPEGKIDRASPASML----VSAYNLKD----KVNGELVTTF-----E 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 GVVGTAAESTINPGDKIDGGAG----NDVLKVDLKNŃ----FKGLKD---DGYIKNIEKL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 SLTNSSVSNRTFDAKGIDGLQTVALSGEKGISVTNLANIVDVEVNGFKGTNFNVDSIYAD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 KVLD-GSADVQNLKVNGVGAKGASVAITADKIETLNLNTTGSQSFVSADVASISVKGNAN 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 VSRAEAAQFIALTDKKYGKKDNA----QAYVTDVKVSEPTKLTLTGTGLDKLSADDVTLE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | : | | : | | : | 386 LSLATGAKTTTLDASSFGGALDADLSTSASVTSIK------GGNGNDKITIKDVAVN 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GDKAVAIEASTDGT-----SAVVTLGGKVAPNKDLTVKVKNQSFVTKFVYE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 VAIDGGAGNDELVIKGSTADTLOPTLTNIEKVTIDGN----TKDLTLSLKKAQSVTELSFK 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --VKKLAVEKLTFDDDRAGQAIAFKLNDEKG-NADVEYLNLANH 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             554 ATELTINSNKVTLASDAVVQAANATKIDINAAKDTVGLTLGG-----VAKLTDLTVNNK 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 GAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDENAQPSFKDAKNIWSSKYIAAVEKA 84
surface-array protein homolog sapA2 - Campylobacter fetus (strain 82-40 LP3)
                               Species: Campylobacter fetus
Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 DLLDHWGEEKANILIN----LGISVG-TGGKWEP-------
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b. 5.5%; Score 231.5; DB 2; Length 2059; Similarity 21.4%; Pred. No. 0.0075; Similarity 21.4%; Pred. No. 0.0075; Similarity 21.4%; Pred. No. 0.0075; Similarity 21.4%; Pred. No. 0.0076; Similarity 2.007YGPTESIDRASANIFTKILNLPVDENAQPSFKDAKNIWSSKYIAAVEKAGVVKG 89	8-Jul-2001 #text_change 18-Jul-2001 Kurokawa, K.; Ishii, K.; Yokoyama, K.; H Shiba, T.; Hattori, M.; Shinagawa, H. erohemorrhagic Escherichia coli 0157:H7

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A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B99789
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1268 <HAY>
A;Experimental source: GB:BA000007; PIDN:BAB34705.1; PID:g13360742; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
A;Genetics:
A;Gene: ECS1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 GQIRGGYVGLES----AALNNNNGD------IQTTGDIAI-ISNGN-----VDNN 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                711 SSCTMID-----NWATGFIASDKNLSLE----VVNSLTNYGWISGKGDVDVTVNNGNLY 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 SADELNVVAGNNYVNAAGQVTGSVSATGSRNGY---SVDVAKLGGMYA-----NKIS-- 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GTLDNTTGTVTSVGTISLNTNKRTIVNT----RAGNISINGD-IYVNSGTIDNTN-- 348
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                                                                                                                                                                                                                                                                                                                                                                                                  PDIODDKLA----GYSVNGGTITLGK-----LDNASP----TEILSRNVVVNGKV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 SFKDAKNIWSSKYI-AAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 LVTTFEDLLDHWGEEKANILINLGI-----SVGTGGKWEPNKSVSRAEAAQFIALTDKK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 YGKKDNAQAYVTDV-KVSEPT-KLTLTGTGLDKLSADDVTLEGDKAVAIEAST-DGTSAV 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             821 --NNRGNIVSDADL-----NVTTKGNLYNYLYMVGYGDIALSANSVANNNATIEATG 870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 VTLGGKVAPNKDLTVKVKNQSFVTKFVYEVKKLAVEKLTFDDDRAGQAIAFK---LNDEK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 NARGSIENRDGNNFG-NAYGLYFGMPQQTGGMVGKEGIELSGQNIYNNNSRLIAEDGPLT 659
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                                                                                                                                                                                                                                                  Query Match 5.5%; Score 231; DB 2; Length 1268; Best Local Similarity 21.9%; Pred. No. 0.004; Matches 200; Conservative 139; Mismatches 358; Indels 218;
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Cyaccesion: E85549

Riperna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001

A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Reference properties of the colimitary A; Mayolecule type: DNA

A; Molecule type: DNA

A; Residues: 1-1270 < STO>

A; Cross-references: GB:AE005174; NID:912514410; PIDN:AAG55657.1; GSPDB:GN00145; UWGP:Z1

A; Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                               hypothetical protein 21542 [imported] - Escherichia coli (strain O157:H7, substrain EDL
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 LVST-----EKGVGVRNLGVIAGGVNGVSIDSKGNLLNSNAQIQSASTINLTTN- 300
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al Similarity 21.9%; Pred. No. 0.004;
200; Conservative 139; Mismatches 358; Indels 218; Gaps
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Db 1173 TYQVSGLKRADTAGSILTGGIARAAGENVGVYGINQGDLAIANSGNYDLSYQGN 1225 Qy 412 KASINKLVATIAGEDKVVDP	OY 653 VGNKVVVT	Search completed: April 7, 2004, 17:33:00 Job time : 29 secs
CO LSKYTSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVVTGKTPGKVDIHLF-KNGATA 678 713 SSGTMIDNNATGFIASDKNLSLEVVNSLINYGMISGKGDVDVTVNNGNLY 762 COY 679 GKATVEIVOETIAIKSV-NEKPV	RESULT 15 F9306 hypotreial protein PA4625 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: F33068 C;Accession: F33068 R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Olson, M.Y. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon, Richession: R83068 A;Accession: R83068 A;Accession: PR3068 A;Accession: PR3068 A;Accession: PR3068 A;Accession: Cipathonary A;Accession: Cipathonary A;Accession: Cipathonary A;Cross-reference retrain PA01 C;Genetics: A;Gene: PA4625	Query Match 5.5% Score 230.5; DB 2; Length 2154; Best Local Similarity 22.3%; Pred. No. 0.0089; Matches 216; Conservative 112; Mismatches 327; Indels 313; Gaps 49; QY 43 RASAAVIFTKILNLPVDEANINSERYIAAVEKAGUVAGDCKENFYBEGKID 102 Db 864 QATASTATQASNVGQYAITGNANGSERFSQRYQLVRQDGKELTVTP

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(without alignments)
5153.464 Million cell updates/sec
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                                                                                                     April 7, 2004, 17:24:49; Search time 51 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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sp_virus: *
sp_vertebrate: *
sp_unclassified: *
sp_rvirus: *
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sp_human:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Д	09red0 bacillus th	Ogzess bacillus th		O81uh4 bacillus an	O81857 bacillus an	O813ke bacillus ce	OBkyes bacillus an	OBlu01 bacillus an	bacillus	O81an7 bacillus ce	O81hb4 bacillus ce	O91655 bacillus ps	045664 bacillus st			Oskrrl figobacteri
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SUMMARIES		1			,							-					
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de	Query Match	18.2	17.4	16.8	13.4	13.2	12.6	12.6	12.1	12.0	12.0	11.3	4.	8.7	7.7	7.3	6.7
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90 GAKPSFKDAQDSWAAKYLAAVEQAGVIQGDGTGNFNPSNQINRASMASMIVKAYKLEDKV 149
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Best Local Similarity 32.7%; Pred. No. 2.5e-23;
Matches 28%; Conservative 11%; Mismatches 316; Indels 155; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAINMERE 4045;

MEDITRE-2120765; PubMed=11320137;

MEDITRE-2120765; PubMed=11320137;

MESTAGE S. 1 Austant M., Fouet A.;

"A general strategy for identification of S-layer genes in the Bacillus crevers group; molecular characterization of such a gene in Bacillus thuringiensis subject-galleriae MRRL 4045.";

Microbiology 147:134-1357(2001)

Microbiology 147:134-1357(2001)

Pigm.; PF00395; SLH; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL 1 29
SEQUENCE 821 AA; 87279 MW; 8D68995C812214B8 CRC64;
                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                          821 AA.
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                         Surface-layer protein precursor.
                                                                                          PRELIMINARY;
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                                                                                                                                               Q9REDO;
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RESULT 1
                                          Q9RED0
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613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 KYTVKDENGTEVV------SPAGIBFVTPAARKINAKGEITLAKGTS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NAQPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENPYPEGKIDRASFASMLVSAYNLKDKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 G----KKDNAQAYVŢ---DVKVSEPTKLTLTGTGLDKLSADDVTL----EGDKAVA--IE 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 ASTDGTSAVVTLGGKVAPNKDLTVKVK--NQSFVTKFVYEVKKLAVEKLTFDDDRAGQAI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 LSEDKKSATVELYSNLAAKQTYTVDVNKVGKVEVTVGSLEAKTIEMADQTVVADEP-TAL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 KVEVQVTKRGGLTVSNTGIITVKNLDTPASAIKN-VVFALDAD------NDGVV---N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391 YGSKLSGKDFALNSQNLVVGEKASLNKLVATIAGEDKVVDPGSISIKSSNHGIISV---- 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 VSVQVELKDOFNNVNNVKABYESLNTEVAVV---DKAT--GKVTVLSAGKAPVKVTVKD 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 -----VNNYITAEA-AGEATLTIKVGDVTKDVKFKVTTDSRKLVSVKANPDKLQVVQNK 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      724 DDIVKGINLTKETQHKVRVVKSGAEQGKLYLDRNGDAVFNAG----DVKL----GDVTVS 775
                                                                                                                                                                                                                                                                                                                                                                       30 AGKSFPDVPADHWGIDSINYLVEKGAVTGNDKGMFEPGKELTRAEAATWMAQILNLPIDK 89
                                                                                                                                                                                                                                                                                                                         1 AGKSFPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         520 --PV----LDQYGKEFAAPVEV--KVLDKDGKELKRQKLVAKYENKEL----VLNAHGQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 AFKLNDEKGNADVEYLNLANHDVKFVANNLDGSPANI-FEGGEATSTTGKLAVGIKQGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 TIVKAVYKKDGKVVAESKEVKVSAEGTAVASISNWTVAÄEKÄDFISKDFKQNDKVYEGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 SKGKELVSKTVETEAFAQKAMKEİKLEKTNVALSTKDVTDFK----VKA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 TLPVTFVTTDQYGDPFGANTAAIKEVLPKTGVVAEGGLDVVTTDSGSIGTKTIGVTGNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     560 GEGTVHFQNGNGATLGSLYVNVTEGNVAFKNFELVSKVGQYGQSPD--TKLDLNVSTTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      618 YQLSKYTSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVVTGK-----TPGKVDIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         608 NELDKYVTEENKKNEMVVSVLPVDANGLVLREKEAATLKVTTTDKDGKVVDATSGQVAVN
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                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                        17.4%; Score 730.5; DB 2; Length 816;
Similarity 30.6%; Pred. No. 6.4e-22;
59; Conservative 119; Mismatches 321; Indels 169;
                                                                                                                                                                          816 AA; 87293 MW; 1002B92905802151 CRC64;
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InterPro, IPR003343; Big_2.
InterPro, IPR008964; Invasin_intimin.
InterPro, IPR001119; SLH.
                                                                   Pfam, PF02368; Big_2; 1.
Pfam, PF00395; SLH; 3.
SMART; SM00635; BID_2; 1.
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                                                      KDNAQAYVIDVKVSEPIKLILI-GIGL-DKLSADDVTLEGDKAV---AIEASIDGISAVV 235
                                                                                                                                                                                                                                                268 TLKNAL------VNKQAYVA-HVKDVKSVDGKDIPKALBVIFFNDEVAPTVSTVF 317
                                                                                                                                                                                                                                                                                                                                                                                                                346 VQVTKRGGLIVSNT----GIIIVK-NLDIPASAIKNVVFALDADNDGVVNYGSKLSGKD 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 GANTAAIKEVLPKTGVVAEGGLDVVTTDSGSIGTKTIGVTGNDVGEG--TVHFQ-NGN-- 570
                121 NGELVTTFEDLLDHWGEEKANILINIGISVGTGGKWEPNKSVSRAEAAQPIALTDKKYGK 180
                                                                                                                                                               210 K--AEAKVESIKEINAKEIEVKFGTEVKDVTAANFAVVEGSKELDIEKVELSKDKKSATI 267
                                                                                                                                                                                                                236 TLGGKVAPNKDLTVKVKNQSFVTKFVYEVKKL-----AVEKLTFDDDRAGQAIAFKLN 288
                                                                                                                                                                                                                                                                                                                    DEKGNADVEYLNLANHDVKFVANN---LDGSPANIFEGGEATSTIGKLAVGIKQGDYKVE 345
                                                                                                                                                                                                                                                                                                                                                               318 D--GNVKVVFSEKLSKDAVTVVINGKEFTATP----BENTVTLTKADVASVVKNGE-AFN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 VIVIGAKDL-VGNIMEMYEGKATYKVEKDVTAPEVKDI--KVKELVDGVATLEVTFSEE- 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400 FALNSQNLVVGEKASLNKLVATIAGEDKVVDPGSISI-KSSNHGIISVVNNYITAEAAGE 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATLIIK-VG--DVIKDVKFKVTIDSRKLVSVKANPDKLQVVQNKTLPVTFVTTDQYGDPF 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523 -----KEV----TAQEGKLRVINLDTSKDVTKEVAVASVEDNKKAITLIFQEKGNYK 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           571 -GATLGSLYVNVTEGN--VAF-KNFELVSKVGQYGQSPDTKLD--LNVSTTVEYQLSKYT 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           672 -----TKNGATAGKATVEIVQETIAIKSVNFKPVQTENFVEKKINIGTVLELEK 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           471 ANLKVEFVGYKDAANNVGNKVTKEVKVTKDVVA-PNLVKVVADBNKAATF-TFD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CTC;
Sun M., Yu Z.;
"S-layer protein gene of Bacillus thuringiensis CTC.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ012290; CAA09981.1; -
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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EMBL; AE017027; AAP24895.1; -.
TIGR; BA0898; -.
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Pfam; PF00395; SLH; 3.
SMART; SM00646; Ami_3; 1.
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Matches 172; Conserv
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16.8%; Score 706; DB 2; Length 823;
Best Local Similarity 30.0%; Pred. No. 6.4e-21;
Matches 272; Conservative 105; Mismatches 309; Indels 222;
                                                                                                                                                                                                                                                         Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428,
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Bacillus thuringiensis subsp. mexicanensis TKD2-14.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
EMBL; D86346; BAA13073.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87602 MW; 96FA83B36A8BACE7 CRC64;
                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                               823 AA
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Pfam; PF00395; SLH; 3.
SEQUENCE 823 AA; 87602
                                                               PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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61 NAQPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKV 120
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645 LAVADAKIVGNKVVVTGKTPGKVDIHLT-------KNGATAGKATVEIV 686
                                                                                                                                                                                                                                                                                                                                                                                                       760 KADATABAAK-----DVVLKVTAPTDVNLATGTVTVKAKELENNAK---YEFKTTDKA 809
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Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
Read T.D., Peterson S.N., Tourasse N., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
Eneson W.C., Peterson J.D., Pop M., Chouri H.M., Radune D.H.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Warkins K.L., Nierman W.C.,
Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Fraser C.M.,
Fraser C.M.,
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                                                                                                                                               651 YILAGAKLPBGTLIVLDGİKALIELPSİFTPEKSETVKFTVANVANKDĞVKMĞ--İANLL
                                                                                                                                                                                                               687 QETIAIKSVNEKPVQTENEVEKKINIGTVLELEKSNLDDI-----VKGINLTKETQHKVR
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InterPro; IPR002558; Amidase_3.
InterPro; IPR001199; Amidase_3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 529;
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32.6%; Pred. No. 2e-15;
tive 81; Mismatches 192; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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S FPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDENAQP
                                                                                                                                                                                                   146 TPATKFKDLETLNWGKEKANILVELGISVGTGDKWEPKKILTKAEAAQFIKKADSLKVGN
                                                                                                                                                                                                                                                                                                                                                                                                                                181 KDNAQAYVTDV-----KVSEPTKLTL-TGTGLDKLSADDVTLEGDKAVAI--EA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 GNPGSNKNESIANRVKFGQENNADIFVSIHANSSEKHDGHGTETYYYKKSKRGEETQIEK
                                                          QPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNG
                                                                                                                                                                                                                                                                                           123 ELVTTFEDLLD-HWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDK-KYGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 STDGTSAVVTLGGKV----APNKDLTVKV----KNOSFVTKFVYEVKKLAVEKLTFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 DRAGQAIAFKINDEKGNADVEYINLANHDVK----FVANNLDGSPA-----NIFE
                      KSPPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDENA
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
S-layer protein / peptidoglycan endo-beta-N-acetylglucosaminidase
(EC 3.2.1.-).
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Best Local Similarity 31.3%; Pred. No. 5.1e-14;
Matches 147; Conservative 70; Mismatches 145; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frank, SW00047; LYZ2; 1.
Glycosidase; Hydrolase; Complete proteome.
SEOUENCE 483 Aa; 53801 MW; 13DOCCA1F2911A6D CRC64;
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EMBL; AE017006; AAP09426.1; -..
EMBL; AE017006; Ramidase activity; IEA.
GO:00040404; F:amidase activity, acting on
GO; GO:0016798; F:hydrolase activity, acting on
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005253; P:peptidoglycan catabolism; IEA.
InterPro; IPR002901; Amidase 4.
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376 NGKLATESGR 385
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                                                                                                                                                                                                                                                                                                                                        240 QRADĞWLKIVTSKĞEKWTP---LTEKTETINEEFTT---YETASHSSKVLGTYNAQTVTV 293
                                                                                                                                                                                                                                                                                                                                                                                                              277 -DRAGQAIAFKLNDEKGNADVBYLNLANHDVKFVANNLDGSPANIFEGGEATSTTGKLAV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 MEESGSWIRIRVGAGFQWVDKNQLNPVKQE----NFLEGK-AIIIDPGHGGIDSGNVGY 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIKQGDYKVEVQV-----TKRGGLTVSNTGIITVK-NLDTPASAIKNVVFALDADNDGV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408 VSIHANGSAEKNGQGTETLYYQSARAKVTNPHVEDSKLLA----QKIQDRLVAALGTKD 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Read T.D., Peterson S.N., Tourasse, N., Baillie L.W., Paulsen I.T., Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple B.K., Okstad O.A., Helgason E., Rilstone J., Mu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R.J., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Berry K.J., Plaut R.D., Wolf A.M., Warkins K.L., Nierman W.C., Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
                                            NGELVTTFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTD----
                                                                                                                                 --KKYGKKDNAQAY------VTDVKVSEPTXLILTGTGLDKLSADDVTLEGDKAVAIE
                                                                                                                                                                                                                                                                     ASTDGTSAVVT-LGGKVAPNKDLTVKVK--NQSFVTKFVYBVKKLAVEKL-TFDD-----
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O: GO:0008253; P:Peptidoglycan catabolism; IEA.
InterPro: IPR002508; Amidase_3.
InterPro: IPR001119; SIM.
Pfam; PP001220; Amidase_3; 1.
Pfam; PF001220; Amidase_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 13.2%; Score 556.5; DB 16; Length 414; Best Local Similarity 39.2%; Pred. No. 3.1e-15; Matches 145; Conservative 54; Mismatches 120; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 HGIISVVNNYITAEAAGEATLTIKVGDVTKDVKFKVTTDSRKLVSVKA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463 RG-VKHQDLYVTRENTMPAVLTELAFVDNKSDADKIATPKORQAAAEA 509
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=198094;
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
N-acetylmuramoyl-L-alanine amidase, family 3.
                                                                                                                                                                             |- : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | :
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MEDLINE=22608414; PubMed=12721629;
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EMBL; AE017029; AAP25724.1; -.
TIGR; BA1817; -.
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SEQUENCE 414 AA;
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257 DKWTPLYEKRETI---HSTFTTYPEASHSSKVLGT-----HSPQTVT--VIEEKGSW 303
                                                                                                                                                                                                                                                                                                                                                                                                        293 -----NADVEYLNLANHDVKFVANNLDGSPANIFEGGEATSTTGKLAVGIKQGD---YKVE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                       346 VQVTKRGGLTVSNTGIITVKNLDTPA----SAIKNVVFALDADNDGVVN------ 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 VRVQKLFAQKTPFTALLTRDAYSRFGKNATDSLGKRVEFAKKNKGDIFVSIHANGFNGNA 423
                                            88 KPSFQDAKNHWASPYIAAVEKAGVIYGDGSGNFNPSKDIDRASMASMLVBAYKLNNRIIG 147
                                                                                                                                                                                                         183 NAQAYVTD---VKVSEPTKLTLTGTGLDKLSADDVTLEGDKAVAIEASTDGTSAVVT-LG 238
                                                                                                                                                                                                                                                        206 TSKRWYMNRHFITYHQP---SLSSGVTSNQHAPQI-----IVVKEQRADGWIKIVTNIG 256
                                                                                                                                                                                                                                                                                                         239 GKVAP--NKDLTVKVKNQSFVT--KFVYEVKKLAVEKLTFDDDRAGQAIAFKLNDEKG-- 292
             OPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=22668414; PubMed=12721629;
Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
Nelson K.E., Tetrelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okerad O.A., Helgason E., Riletone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Hazen A., Cline R., Wolf A.M., Watkins K.L., Nierman W.C.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
                                                                                                                                       123 ELVITFEDILDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 HGTETFYYKAPTQKSNPYVNDSRILAEKIQ-KRLITALQTRDRGVKIGNLYVLREN 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 -----YGSKLSGKDFALNSQNLVVGEKASLNKLVATIAGEDKVVDPGSISIKSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome sequence of Bacillus anthracis Ames and comparison
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12.1%; Score 509; DB 16; Length 344;
Best Local Similarity 59.9%; Pred. No. 2e-13;
Matches 103; Conservative 22; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=198094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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InterPro; IPR001119; SLH.
Pfam; PF05031; NEAT; 1.
Pfam; PF00395; SLH; 3.
Complete proceome.
SEQUENCE 344 AA; 38277 MW; 4876
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EMBL; AE017027; AAP25072.1; -.
TIGR; BA1093; -.
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(TrEMBLrel. 24, L
(TrEMBLrel. 25, L
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01-OCT-2003
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                                                                         125 VTTFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGKKDNA 184
                                                                                                                                                                       QAYVT----DVKVSEPTKLT-------LTGTGLDKLSADD---VTLEGDK 220
                                                                                                                                                                                                                                                                             AHAILESGYGKSEIAYQKHNIFGLRAYDGDPPKYAKYLPSYGDSIAYNANYVRERYLEES 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 GMYYNGSTLIGMNVKYASDKGWAKKIAGIMERIKPFRVEDYTY------AKKLPKNP 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATSTTGKLAVGIKQGDYKVEVQVTKR 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGEL 124
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                                                                                                                                                                                                                                                                                                                                           21 AVAIEASTDGTSAVV--------TGGKVAPNKD------
FPDVPT--WADKSVNYLVDKQVLNGYPDGTFGSNDSLDRASATKIMTKVLGIKIDPNAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=A2012;
MEDLINE=22061436; PubMed=12004073;
Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
Keim P., Fraser C.M.;
"Comparative Genome Sequencing for Discovery of Novel Polymorphisms:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus anthracis.";
Science 256:2028-2033(2002).
EMBL; AR011191; AAM26204.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity;
GO; GO:0009253; P:peptidoglycan catabolism; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 GGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDF 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (pX02-42)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Surface-layer N-acetylmuramoyl-L-alanine amidase, (I
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InterPro; IPR001119; SLH.
Pfam; PF01520; Amidase_3; 1.
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Plasmid pXO2.
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65 SFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGEL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OVKPEDLKGHWGEKYANILIGLKISNGTENGWQPNRFITRAEAAQLTAKTDMMQHRQKN 205
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I. Nature 423:87-91(2003).

B. REMEJ, ARD17009; AAP10458.1; -.

B. REMEJ, ARD17009; AAP10458.1; -.

B. GO; GO:0016787; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:00098745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0009875; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0009875; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0009875; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.

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BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine activity; IEA.

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BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine activity; IEA.

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BR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine activity; IEA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDENAQP
                                                                                                                                                                         282 AIAF--KLNDEKGNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATSTTGKLAVGIKQ
                                                                                                                                                                                                                                                 304 ETYYYKSSKSEKTNPHVE-----ESRVLAEKIQTRLV-----DALQTRDR---GVKH
                                                                                                 253 FT-VLLTRKSDTRPGHDQKSSLQERVKFAKQNQGDIF-----ISVHANAFNGNAKGT
                     GTSAVVTLGGKVAPNKD----LTVKVK----NQSFVTKFVYEVKKLAVEKLTFDDDRAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=22608415; PubMed=12721630;
MEDIINE=22608415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Ivanova N., Sorokin A., Anderson I., Galleron N., Lapidus A.,
Kapatral V., Bhatacharya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.;
Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                     GDYKVEVQVTKRGGLTVSNTGIITVKN-LDTPASAIKN-VVFALDADNDGVVNY 391
                                                                                                                                                                                                                                                                                                                                                                                    | | : | : | : | : | : | GD----LHVIRENDMPAVLTELAFIDNGIDYSKLSTENGRQIAAEAIYEGILDY 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-010N-2003 (TrEMBLrel. 24, Created)
01-010N-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
S-layer protein / N-acetylmuramcyl-L-alanine amidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
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Best Local Similarity 54.77
Matches 98; Conservative
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Q81HB4;
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Q81HB4
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Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
Benton J.L., Mahamoud Y., Jang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Warkins K.L., Nierman W.C.,
Thomason B., Zline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Fraser C.M., Hanna P.C., Kolsto A.-B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 PPDVPAGHWAEGSINYLVDKGALTGKPDGTYGPTESIDRASAAVIFTKILNLPVDENAQP
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                                                                                                                                                                                                      FPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDENAQP
                                                  SFXDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGEL
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                                                                                                                                                                                                                                                                                                                        125 VITFEDLIDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAOFIALTDK 176
                                                                                                                                                                                                                                                                                                                                                                   287 PKEFADLNNHWGAKYANILIQEKISIGTDNGWAPNKAVSRAEAAQFIAKADK 338
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12.0%; Score 506; DB 16; Length 4:
Best Local Similarity 34.1%; Pred. No. 3.4e-13;
Matches 141; Conservative 62; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=198094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28F7F51302F92428 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 AA
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Nature 423:81-86(2003).
EMBL; AB017032; AAP26383.1; -..
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Pfam; PF00395; SLH; 3.
SMART; SN00646; Ami 3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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GO, GO:0016787; F:hydrolase activity; IEA.

GO, GO:0001455; F:hydrolase activity; IEA.

GO, GO:0001455; P:nacetylmuramoyl-L-alamine amidase activity; IEA.

GO; GO:0009253; P:peptidoglycan catabolism; IEA.

InterPro; IPR001119; SLH.

InterPro; IPR001119; SLH.

Pfam; PF01520; Amidase_3; 1.

Pfam; PF01520; Amidase_3; 1.

Pfam; PF001520; Amidase_3; 1.

Hydrolase; SGO0646; Ami 3: 1.

Hydrolase; Complete protecome.

SEQUENCE 530 AA; 58834 MM; 37E448FB109D2598 CRC64;
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Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
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"Genome sequence of Bacillus cereus and comparative analysis with
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                                                                  (EC
                                                                                                                                                      Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=226900;
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
S-layer protein / N-acetylmuramoyl-L-alanine amidase
3.5.1.28).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 ADNDGVV--NYGSKLSGKDFALNSQNLVVGEKA---SLNKL-----VAT----IA
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Rendrick N., Krulwich T.A.;

"Two-Dimensional Gel Electrophoresis Analyses of pH-Dependent Protein

"Two-Dimensional Gel Electrophoresis Analyses of ph-Dependent Protein

Expression in Facultatively Alkaliphilic Bacillus pseudofirmus OF4

Lead to Characterization of an S-Layer Protein with a Role in
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9.4%; Score 395; DB 2; Length 931;
Best Local Similarity 24.2%; Pred. No. 3.2e-08;
Matches 233; Conservative 106; Mismatches 336; Indels 288; Gaps
                                                                                                                                                   Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=79885;
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J. Bacteriol. 182:5969-5981(2000).
EMBL; AF742295; AAF68436.1;
Inter-Pro; IPRO01119; SLH.
Pfam; PRO0395; SLH; 3.
SEQUENCE 931 AA; 96855 MW; 6A9727171C0A78D0 CRC64;
                                          Created)
Last sequence update)
Last annotation update)
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931
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527 GVNQKTIKVSAV--DQYG-----KEI--KFGT---KGKVTVTTNTEGLVIKNVN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   854 FSLANVVKTGSGTVSSS-----PSLSDAI--QLTNSGDAVSFTLVIKSIYVKGADK
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                   LVTTFEDLLDHWGEEKANILINLGISVG-TGGKWEPNKSVSRAEAAQFIALTDKKYGKKD
                                                                            : | |: | |: | |: | | : | | : | 147 VKLPFTDVNDTWA-PYVKALXKYEVTKGKTPTSFGAYQNITRGDFAQFVY-----RAV
                                                                                                                      NAQAYVTDVKVSEPTKLTLTGTGLDKLSADDVT-LEGDKAVAIEAST---DGTSAVVTLG
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                                                                                                                                                                                239 GKVAPNKDLTVK---VKN-----QSFVTKFVYEVKKLAVEKLTFDDDRAGQAIAFKLND
                                                                                                                                                                                                          KPFTRNQEYTITATGIKNLKGETAKELTGKFVWSVQDAVTVALNNSSLKVGEESGLTVKD
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-0CT-2002 (TrEMBLrel. 22, Last ann
Surface layer protein precursor.
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                                                   - FITTASLNHNNFKIDGQAVSSN----SDITLNSTRDIITVSLPSEDSVKISGNALFTIN
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                                                                                            570 -NGATLGSLYVNVTEG:--NVAFKN-----FELVSKVGQYGQSPDTKLDLNVSTTVEYQL
                                                                                                                                                      SKYTSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVVTGKTPGKVDIHL-----TKN
                                                                                                                                                                                                                  G-----ATAGKATVEIVQETIAIKSVNFKPVQTENFVEKKINIGTVLELEKSNLD-
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                                AAIKEVLPKTG------VVAEGGLDVVTTDSGSIGTKTIGVTGN-DVGEGTVHFQNG--
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MEDLINE-97197531; PubMed-9045827;
Ruen B., Koch A., Asenbauer E., Sara M., Lubitz W.;
Kuen B., Koch A., Asenbauer E., Sara M., Lubitz W.;
Wolecular characterization of the Bacillus stearothermophilus PV72
layer gene sbsB induced by oxidative stress.";
J. Bacteriol. 179:1664-1670(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
Local Similarity 23.3%; Pred. No. 4.4e-07;
Les 227; Conservative 138; Mismatches 369; Indels 240;
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Geobacillus
   NNKNDLYSKSITLNKDTVAPTVTSAALASNRQAIEVTLSEGVTIT-
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97916 MW; 1F3C20344B40F3A2 CRC64;
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AR-2003 (TrEMBLrel. 23, Last annotation update)
gene (Sequence 5 from PATENT W09906567 precursor)
                                                                                                                         694 NNAVNAPSVSVSATPAAPLNVAVANSGTNVFTVTAPTGQ----
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Lubitz W., Resch S.;
EXTRACELLULAR SPACE.";
Patent number W09906567-A/5, 11-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                920 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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EMBL; AX000222; CAB77070.1; --
InterPro; IPR001343; Big_2.
InterPro; IPR01119; SLH.
Pfam; PF00396; SLH; 3.
SMART; SM00635; BID_2; 2.
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SEQUENCE FROM N.A.
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NCBI_TaxID=1422;
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01-MAR-2003
SBSB gene (Se
SBSB.
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01-NOV-1996
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Best Local S
Matches 227
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102 AVNPLKEAGIISGKTATEFKPDANITRGEMAIIVAKAYKIQAVASKEV--PFKDATGIYK 159
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STRAINs_deang 1995;
MEDILINE=95291197; PubMed=7539663;
Jeang C.L., Lee Y.H., Chang L.W.;
"Purification and characterization of a raw-starch digesting amylase from a soil bacterium--fytophaga sp.";
Biochem. Mol. Biol. Int. 35:549-557(1995).
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                                                                                                                                                                                                                                                                                                                              OSRBS;
01-YAY-2000 (TEMBLE1. 13, Created)
01-YAY-2000 (TEMBLE1. 13, Last sequence update)
01-UN-2003 (TEMBLE1. 24, Last annotation update)
5-layer protein precursor.
Cytophaga sp. Jeang 1995'.
Bacteria, Bacteroidetes; Sphingobacteria; Sphingobacteriales;
Flexibacteraceae; Cytophaga.
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STRAIN=Jeang 1995;
STRAIN=Jeang C.L., Liao T.W., Chiou S.Y., Kang P.L., Shieh T.Y.,
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF068060; AAF21259.1; -.
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47 S-LAYER PROTEIN.
108718 MW; 4395402E9965295A CRC64;
                                                                                755 DRNGDA--VFNAGDVKLG-----DVTVSQTSDSAL----PNFKA
                                                                                                                        7.3%; Score 307.5; DB 2;
0.8%; Pred. No. 0.00014;
ve 153; Mismatches 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF068060, AAF21259.1; -.
GO, GO:001620; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
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Pfam; PF00395; SLH; 3.
Pfam; SN00635; BID 2; 2.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
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InterPro; IPR000515; BPD transp.
InterPro; IPR001119; SLH.
                       --TLNPGT
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33 104
1047 AA;
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Matches 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LDHWGEEKANILINLGISVGT--GGK--WEPNKSVSRAEAAQFIALTDKKYGKKDNAQ 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                            IIk N., Egelseer E.M., Jarosch M., Sleytr U.B., Sara M.; "Nucleotid sequence of sbpA, the S-layer gene from Bacillus sphaericus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VTLDGEEIGKFKGIEAVVPKSIVLKTTNTQG------KVGNQVTLTADV
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23.8%; Pred. No. 4.5e-05;
ive 93; Mismatches 296; Indels 240;
                                                                                                                                                                                                                                                                         CCM 2177.", Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. HSSP, P22629, ISML.
HSSP, P22629, ISML.
InterPro. IPROILI19, SLH.
Pfam, PF00385, SLH; 3.
PROSITE, PS01072; SLH_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 POTENTIAL.
132046 MW; 2C51D40FADFD0886 CRC64;
                                              Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1421;
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1268 AA;
                              sphaericus
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Best Local Similarity
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Wed Apr

Search completed: April 7, 2004, 17:31:54 Job time: 57 secs

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GenCore version 5.1.6
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protein - protein search, using sw model

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April Run on:

7, 2004, 17:19:59 ; Search time 62 Seconds (without alignments) 3796.162 Million cell updates/sec

US-09-844-281-1

Title: Perfect score:

4202 1 AGKSPPDVPAGHWAEGSINY.....ITSEIGSQAVHVNVLNNPNL 833 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

1586107

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A Geneseq 29Jan04:* L: geneseqp1980s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	7 Aam47757 Ma	4651 Amino ac:	7672 Abul7672 Protein	7636 Abu17636 Protein	Abu18750	•	Abu18670 Pro	Aar80530	Aaw22863 Bac	0626 Aab10626 B. stearo	Aaw93253	1 Aar41731	1 Aaw30291 Non-t	S Aar77395	7478 Cellulase	2 Aaw30292 1	Aar41732	3 Aar99393 1	1845 Aab01845 Haemophi	1844 Haemophi	Aab01825	Aab01824	0 Aab23860	1 Pah01841	TERTOCION
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26	27	28	58	30	31	32	33	34	32	36	37	38	39	40	41	4	43	4.4	45

ALIGNMENTS

AAM47757 standard; protein; 833 AA. RESULT 1

AAM47757;

(first entry) 25-FEB-2002

Mature EA1 protein.

Anthrax; antibacterial; vaccine; EA1 antigen.

Bacillus anthracis.

WO200183561-A2.

08-NOV-2001.

30-APR-2001; 2001WO-US013648.

28-APR-2000; 2000US-0200505P.

(TETR-) TETRACORE LLC

O'brien TW; Aldrich JL, Mangold BL,

WPI; 2002-055457/07.

Novel monoclonal antibody, useful for detecting B.anthracis, and for treating B.anthracis infection, is specifically reactive against Bacillus anthracis and is non-reactive with B.thuringinesis and B.cereus.

Claim 6; Fig 1; 27pp; English.

The present invention relates to a monoclonal antibody which is specifically reactive against Bacillus anthracis EA1 antigen. The present sequence is the mature EA1 protein from Bacillus anthracis. The EA1 protein corresponds to the eag gene. The monoclonal antibody is highly specific for Bacillus anthracis, and can distinguish Bacillus anthracis from closesly related non-pathogenic species. The present sequence is useful for producing a vaccine against Bacillus anthracis and the antibody is useful for treating, preventing or controlling Bacillus antibody is useful for treati anthracis infection (anthrax)

Sequence 833 AA;

Length 833; Score 4202; DB 5; Pred. No. 2.2e-238; 100.0%; Query Match Best Local Similarity

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                                                                          NAQPSFKDAKN1WSSKY1AAVEKAGVVKGDGKENFYPEGK1DRASFASMLVSAYNLKDKV
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                                                                                                                                                                                                                                        \mathsf{the}
                        nucleotides
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Location/Qualifiers
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                                                                                                         04-JAN-2001; 2001WO-US000358
                                                                                                                                06-JAN-2000; 2000US-0174901P
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233; Conservative
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N-PSDB; AAH28330.
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  Key
Misc-difference
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                                                                                  12-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                    638
                                                                                                                                                                          725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
VKVTVKDSKGKALVSHTVEIBAFAQKAMKDIKLEKTNVA---LSTKDVTD------L 485
                                                          539
                                                                                ECTVHF -- QNGNGATLGSLYVNVTEGNVAFKNFELVSKVGQYGQSPDTKLDLNVSTTVEY 618
                                                                                                                                                                                                                                                                                                                                                                                              prokaryotic essential gene; cell proliferation; drug design.
                                                     486 KVRAPVIDQYGKEFTAPVTV--KVIDKDGKEIKEQKLBAKYVNREIV----INAAGQEAG
                                                                                                                                               ---KYVTEENQKNAMTVSVLPVDANGLVLKGAEAAELKVTTTNKEGKEVDATDAQVTVQN
                                                                                                                                                                                       PVTFVTTDQYGDPFGANTAAIKEVLPKTG-VVAEGGLDVVTTDSGSIGTKTIGVTGNDVG
                                                                                                                                                                          --IHLTKNGATAGKA-TVEIVQETIAIKSVNFKPVQTENFVEKKINIGTVLELEKSNLDD
                                                                                                                             619 QLSKYTSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVVTGKTPGKVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind JW;
Xu HH;
                                                                                                      540 NYTVVITAKSGEKEAKATLALEL-KAPGAFSKFEV------RGLDTELD
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                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #3199
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 45596; 1766pp; English.
                                                                                                                                                                                                                                                                                                      ABU17672 standard, protein, 529 AA
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Carr GJ,
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25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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Trawick JD,
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694 VAPNADL 700
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proliferation or the activity of a gene in an operon required for compound that has an activity against a blological pathway required for proliferation, or that has an activity against a blological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound s activity; (11) a culture comprising strains in which the gene or which each of the strains is present in a culture or collection of product is overexpressed or underexpressed; (12) determining the extent of the strains; or (13) identifying the target of a compound that inhibits the complement of an organism. The antisense nucleic acids are useful for graining proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational culture displaying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. required for proliferation in cells other than S. aureus, S. typhimurium, the traget prokaryotic essential genes. Note: The sequence data for this patent did not form part of the prished specification, but was obtained completed province of the prished province of the prished province of the present sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NAQPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 ORADGWLKIVTSKGEKWTP---LTEKTETINEEFTT---YETASHSSKVLGTYNAQTVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 --KKYGKKDNAQAY-----VTDVKVSEPTKLTLTGGGLDKLSADDVTLEGDKAVAIŖ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
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Matches 172; Conservative
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us-09-844-281-1.rag

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Antisense; prokaryotic essential gene; cell proliferation; drug design.
     Protein encoded by Prokaryotic essential gene #3163.
                                                                       06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                        21-MAR-2002; 2002WO-US009107
                                                                                      06-MAR-2002; 2002US-0362699P
                                                                                                 (ELIT-) ELITRA PHARM INC.
                                                                                                           Zamudio C,
Trawick JD,
                                                                                                                         WPI; 2003-029926/02.
N-PSDB; ACA21506.
                         Bacillus anthracis
                                                                                                                                                                                                                                                                                                                                             Sequence 414 AA;
                                   WO200277183-A2.
                                             03-OCT-2002
                                                                                                           Wang L,
Wall D,
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Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R; Yamamoto R,

Malone C, Carr GJ,

C The invention relates to an isolated mucielic acid compitising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promotrer operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated the polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway crequired for proliferation, (7) identifying a cellular proliferation or the biological pathway in which a proliferation required for compound that inhibits encolleration of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene compound, activity; (11) a culture comprising strains in which the gene compound, activity; (11) a culture comprising strains in which the gene compound, activity; (11) a culture comprising strains in which each of the strains is present in a culture or collection of compound the strains; or (13) identifying the target of a compound that inhibits the collection of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, C. the target prokaryotic essential genes. Note: The sequence data for this patent did not form what directly from WIPO at the printed sequence is conded by one of the target promise or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence is conded by one of the target promise or P. aeruginosa. The present sequence is e New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. The invention relates to an isolated nucleic acid comprising any one of Claim 25; SEQ ID NO 45560; 1766pp; English.

Ouery Match
13.2%; Score 556.5; DB 6; Length 414;
Best Local Similarity 39.2%; Pred. No. 1.2e-24;
Matches 145; Conservative 54; Mismatches 120; Indels 51;

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. ELVITFEDLLD-HWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDK-KYGK 180 206 PLVEKVVIIDPGHGGFDPGNPGQGVEBSKIVFDTSLRLQKLLEKNTPL---KALLTREEN 262 DRAGQAIAFKINDEKGNADVEYINLANHDVK-----FVANNLDGSPA-----NIFE 322 D--SEVLAKKIQ----NRVVEALHTRDRKIKDDHSLYVVNN-NTVFAVLTELAFIDNDID 375 146 TPATKFKDLETLAWGKEKANILVELGISVGTGDKWEFKKILTKABAAPIKKADSLKVGN 205 The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated KTPPDVQTGHWAEDSINYLAEKGAVTGNEKGMPEPGKEITRAEAATWMAKILNLPIDKNA 86 Antisense; prokaryotic essential gene; cell proliferation; drug design. GNPGSNKNESLANRVKFGQENNADIFVSIHANSSEKHDGHGTETYYYKKSKRGEETQIEK 181 KDNAQAYVTDV------KVSEPTKLTL-TGTGLDKLSADDVTLEGDKAVAI--EA 227 SIDGISAVVILGGKY----APNKDLIVKY----KNQSFVIKFVYEVKKLAVEKLIFDD QPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNG Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Protein encoded by Prokaryotic essential gene #4277. Haselbeck R, Yamamoto R, claim 25; SEQ ID NO 46674; 1766pp; English. ABU18750 standard; protein; 525 AA. Malone C, Carr GJ, 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2001; 2001US-00815242. 21-MAR-2002; 2002WO-US009107 (first entry) (ELIT-) ELITRA PHARM INC. 323 GGEATSTIGK 332 376 NGKLATESGR 385 Zamudio C, Trawick JD, WPI; 2003-029926/02. N-PSDB; ACA22620. Bacillus anthracis WO200277183-A2. 19-JUN-2003 Wang L, Wall D, 27 87 123 277 323 63 ď ò g ઠે 台 ठ ద Š g ò ద

polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation. The specific pathway in which the test compound that inhibits proliferation of an orangeneon on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; (11) a culture comprising strains in which the extent compound that inhibits in the gene product is overexpressed or underexpressed; (12) determining the extent convict each of the strains is present in a culture or collection of strains or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proceins or screening for homologous nucleic acids required for acidinary proliferation to the soluter candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct sequences

Sequence 525 AA;

61 NAQPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKV 120 138 IGELPTQFKDLEPHWGKKQANILVALEISKGTGNGWNPEGTVTRAEAAQFIAMAEKKIKQ 197 272 LTFDDDRAGQAIAFKLNDEKGNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATSTTG 331 341 NVGYYEKESDTVLDVSLRLKKIIXAKAPFTVMFTRTDNTRPGVNSTDSLKKRVEFAQEHN 400 DDYTLEGDKAVAIEASTDGTSAVVTLGGKVAPNKDLTVKVKNQSFVTKFVYEVKKLAVEK 271 1 AGKSFPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDE 60 77 AAKKFSDVPT -- WAQQSVDYLVGKKALDGKPDGTPSPSEAVDRGSAAKILAVVLGLPVDP KDNAQAY-----VTDV------VVDV------KVSEPTKLTLTGTGLDKLSA----Gaps Query Match
Best Local Similarity 31.8%; Pred. No. 2.5e-24;
Matches 164; Conservative 71; Mismatches 172; Indels 109; 427 KVVDPGSISIKSSNHGIISVVNNYITAEAAGEATLT 121 198 212 301 d δ g g g 셤 엄청 8 8 ò ò ò g ò 8

137 NGELVITTEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGK 180 STSKRMYMTRNVITYHHPSLSSGITDVHHKPQNGKVTEQ-----RADGWVKMLTSKREKW 252 DISNRKNRNDLMKEFSTYGT-----ASHSSKVLGTYNAQTVTVMEKEWKLIRI-- 300 KLAVGIKQGDYKVEVQ-----VTKRGGLTVSNTGIITVK-NLDTPASAIKNVVFALDAD 384 NDGVVNYGSKLSGKDFALNSQNL------VGEVASLNKLVATIAGED 426 480 ----rvtrentlpavlt RGVKHODL 460

ABU17384;

(first entry) 19-JUN-2003 Protein encoded by Prokaryotic essential gene #2911.

Antisense; prokaryotic essential gene; cell proliferation; drug design

Bacillus anthracis.

WO200277183-A2

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, Wang L, Wall D,

WPI; 2003-029926/02. N-PSDB; ACA21254.

screening New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

SEQ ID NO 45308; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated completed or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding can polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway in which a proliferation required gene product or that has an activity against a biological pathway in which the test compound that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture compusing strains in which the test compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation of an organism. The antisense nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids required for a cellular proliferation of an organism. The antisense nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids required for the processed or the strains is processed and the candidate molecules for a capital and an organism of an organism and the candidate molecules for a capital and an organism and the candidate molecules for a capital and an organism and the can by one of for this drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of pneumoniae or P. aeruginosa. The present sequence is encoded by one ce target prokaryotic essential games. Note: The sequence data for this tent did not form part of the printed specification, but was obtained electronic format directly from WIPO at tp.wipo.int/pub/published_pct_sequences

Sequence 379 AA;

Gaps 9.8 Length 379; 10.9%; Score 459; DB 6; Length 37: llarity 32.5%; Pred. No. 5.8e-19; Conservative 49; Mismatches 110; Indels Query Match Best Local Similarity Matches 124; Conserv

13;

ABU17384 standard; protein; 379 AA ABU17384 ID ABU1 XX RESULT 6

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124
                                                                                                VITFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGKKDNA 184
                                                                                                                         192
                                                                                                                                                 QAYVIDVKVSEPIKLTLIGTGLDKLSADDVTLEGDKAVAIEASTDGTSAVVTLGGKVAPN 244
                                                                                                                                                                          ---MLQYSHSNPLE------PG 219
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                                                                                                                                                                                                                            KD-TKGLPXKXIVLDTSLRLQKL-LEKHTPFTVLLNSXSDTRTGHGSKSSL-QERG--- 272
                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell, Also included are:
                                                                      SFKDSONHWGTPYMPAAEKAGSIKVEGKGIFNPSGKVTRAAMATMLVNAYKLONKNTSNG 141
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64
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                FPDVPA--WADKSVTYLVDKQVLSGYPDGTFGSSDTLDRASAATIMTALGIHIDLNAKP
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Xu HH;
                                                                                                                                                                                                  KDLTVKVKNQSFVTKFVYEVKKLAVEKLT------FDDDRAGQAIAFKLNDEKGNADV
FPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDENAQP
                                              SFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGEL
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for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #4197.
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Yamamoto R,
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Carr GJ,
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2001US-0342923P.
2002US-00072851.
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Trawick JD,
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N-PSDB; ACA22540.
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06-SEP-2001; 2
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CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibiting aclated polypeptide or its fragment whose expression is inhibiting cellular cantisense nucleic acid; (4) an antibody capable of specifically binding cellular proliferation or the activity of agene in an operon required for proliferation or the activity of agene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene product is expensed for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sactivity; (11) a culture comprising strains in which the strent compound strains in which the extent or organism; or (13) identifying the target of a compound that inhibits the computed of an organism. The antisense nucleic acids are useful for the strains; or (13) identifying the target of a compound that inhibits collection of cragined for proliferation in cells other than S. aureus, S. typhimurium, C. crugalized for proliferation in cells other than S. aureus, S. typhimurium, C. crugalized for proliferation in cells other than S. aureus, S. typhimurium, C. che target prokaryotic essenting lense. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at C. fips electronic format directly from MIPO at C. fips electronic format directly from MIPO at C. fips electronic format directly from MIPO at C. fips electronic format directly from MIPO at C. fips electronic format directly from was obtained to the target procedul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KSFPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILMLPVDENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 -ELVTTFEDLLDH-WGEEKANIL-INLGISVGTGGKWEPNKS-VSRAEAAQFIALTDKKY
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hes 148;
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AAR80530 standard; protein; 1252

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                             454 VNGVKALQLSN-----GTALDAAQITTDŠK------GEATFTVSGTNAAVTPVVY 497
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                                                                                      473 KFKVTTDSR-----KLVSVKANPDKLQVVQNKTLPVTFVTTDQYGDPFGANTAAIKEV
                                                                                                                                                                                                                                                            ------HFQ----NGNG-----ATLGSLYVNVTEGNVAFKNFELVSKVGQ----
                                                                                                                                                                                                                                                                                           557 EPKAVAPISYFQAPYLDGSAIKAYKKSDLNKAVTKFDGSETAVFAAELVNQSGKKVTGTS
                                                                                                                                                                                                                                                                                                                          -----YGQ-SPDTKLDLNV----STTVEYQLSKYTSDRVYSDPENLEGYEVESKNL
                                                                                                                                                                                                                                                                                                                                                                                           AVADAKIVGNKVVVTG---KTPGKVDIHLIKNGATAG-KATVBIVQETIAIKSVNFKPVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PVKYAGVSGKTYKYFGANG
KNVVFALDADNDGVVNYGSKLSGKDFALNSQNLVVGEKASLNKLVATIAGEDKVVDPGSI
                                                                                                                                                                                            ----IGVTGNDVGEGTV---
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                                                                                                                                                    Bacillus stearothermophilus S-layer protein sbs-B.
                                                                                                                                                                                                526 LPKTGVVAEGG----LDVVTTDSGS----IGTKT--
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/label=_sig_peptide
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/label= mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      820 TQFNTADSGSNSNSIWFAGKN--
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27-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLGGK------VAPNKDLTVKVKNQSFVTKFVYEVKKLAVEKLTFDDDRAGQAIAF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KINDEKGNADVEYLNLANHDVKFVA----NNLDGSPANIFEGG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 TVPGNNNDGVVPTLTGEALTNEEGIATYSYTRYKEGTDEVTAYATGDRSKFSLGYVFWGV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EATSTICKLAVG--IKOG---DYKVEVQVIKRGGLIVS---NIGIIIVKNL--DIPASAI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : :: ; | | ; | | ; | | ; | | ; | | | ; | | | ; | | | ; | | | ; | | | ; | | | ; | | | ; | | DIILSVEEVITGASVANGANKTYKVIYKNPKTGKPEANKTFNVGFVENMNVTSDKVANAT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGELVTTFEDL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 AWYNSIAAVVANGIFEGVSATEFAPNKSITRSEAAKILVEAFGLEGEAD---LSEFADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V----TDVKVS---EPTKLTLTGTGLDKLSADDVTLEGDKAVAIEASTDGTSA----VV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.8%; Score 369; DB 2; Length 1252; Best Local Similarity 22.9%; Pred. No. 5.4e-13; Matches 221; Conservative 131; Mismatches 347; Indels 264; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Host cell expressing surface layer protein fusion protein - used for presentation of antigens and vaccine prodn.
                                                                     layer protein; SLP; fusion protein; vaccine; antigen; expression; epitope.
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/label= Sig_peptide
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        (first
                                                                                                                  Bacillus sphaericus
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                                       B. sphaericus
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        22-DEC-1995
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08-JAN-2001
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                                                                                                   Preparation of S-layer proteins by expressing sbs-A gene in Gram negative bacterium - or new sbs-B gene in any host, also new recombinant proteins containing heterologous inserts, e.g. epitope(8), useful as vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 LVTTFEDLLDHWGE-----EKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 VKLPFTDVNDTWAPYVKALYKYEVTKRLKHQQASVHT-----KNITLRDFAQFVY--- 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 SAVVTLGGKVAPNKDLTVK---VKN----QSFVTKFVYEVKKLAVEKLTFDDDRAGQA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVEVVVNKPFTRNQEYTITATGIKNIKGETAKELTGKFVWSVQDAVTVALNNSSLKVGEE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 IAFKLNDEKGNADVEYLNLANHDVKFVANNLDGSPANI--FEGGEATSTTGKLAVGIKQG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 DYKVEVQVTKRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDF 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 ALNSQNLVVQEKASLNKLVATIAGEDKVV------DPGS-----ISIKSSNHGIIS 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGE 123
                                                                                                                                                                                                   The present sequence is the Bacillus stearothermophilus PV72 S-layer protein, sbs-B. S-layer structures can be used as vaccines or adjuvants, particularly when they include a bacterial ghost that may contain additional epitopes in its membrane. Other uses of recombinant sbs-B, depending on the nature of the inserted peptide, are as an universal carrier for biotinylated reactants for use in immunological or hybridisation assays (the insert is streptavidin), to induce immune responses (epitopes), as a reagent for removing cytokine or toxin from serum (antigenic epitopes), as amolecular spinning nozzle (polyhydroxybutyrate synthase) and as a molecular laser (luciferase). (Updated on 17-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 SFPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDENAQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGFIDVPKD-RAKYVNALVEAGVLNGKAPGKFGAYDPLTRVEMAKIIANRYKLK---ADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 SGLTVKDQDGK------DVVGAKVELTSSNTNIVVVSSGEVSVSAAKV-TAVKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PONTVAENKA--EKVTSMFAGETKTVAMYDTKNGDPETKPVDFKDATVRSLNPIIAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          521 VGGGEVEGVNQKTIKVSAV--DQYG------KEI--KFGT----KGKVTVTINTEGL
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                                                                                                                                                                                Claim 26; Page 19-23; 31pp; German.
                              'n
                           Lubitz W, Sleytr U,
                                                       WPI; 1997-394558/37.
N-PSDB; AAT75488.
(SLEY/) SLEYTR U.
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 921 AA;
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This invention describes a novel host cell (A) comprising at least two befunctional recombinant polypeptides (I), at least one being in carrier bound form. The products of the invention have antibacterial activity.

(A), or, where bacterial, their ghosts (B), are useful as vaccines or adjuvants (specifically for presentation of immunospanic espitopes of pathogens or autologous immunostimulatory polypeptides, e.g. cytokines), or preferably, as enzyme reactors for performing a cascade of reactions, or preferably synthesis of poly(hydroxyalkanoate). Localization of individual (I), specifically enzymes, in separate cellular compartments avoids adverse reactions between products and substrates, when being used
                                                                                    592
                                                                                                                                                                                                                                   667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      593 -DKIVNGKVEVKYFKNASD---TTPTSTKTITVNVVNVK-ADATPVGLDIV----APSKI
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813
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/label= signal_peptide
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/label= mature_peptide
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                                                                                                                                                                                                                                                                                                               146
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                                                                                                                                                                                                                             || || || :: || :| || || || SPIDVAPQY--KDAIDFLVSTGATKGKTETKFGVYDEITRLDAAVILARVLKLDVDNAKD 90
 carrier-bound form without loss
                                                                                                                                                                                                                                                                                                   ---PONTVAFNKA--EKVTSMFAGETKTVAMYDTKNGDPETKPVDFKDATVRSLNPIIAT
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                                                                                                                                                                                                                                                                                                                                                                                                                           176 KKYGKKDNAQAYVIDVKVSEPIKLILIGIGLDKLSADDVI-LEGDKAVAIEASI---DGT
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as bioreactors. (I) can be produced in carrier-bound form without los function. This sequence represents the Bacillus stearchtermophilus S-layer protein sbsB which is used to illustrate the method of the invention. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                209;
                                                                                                                             1 8.7%; Score 367.5; DB 3; Length 921; Similarity 24.9%; Pred. No. 4.4e-13; Conservative 121; Mismatches 335; Indels 209
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                                                                                            Sequence 921 AA
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Matches 220;
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sbsB protein, S-layer protein, Gram-negative, prokaryotic host cell; integration, cytoplasmic membrane, secretion, periplasmic space; toxin, evararyotic host cell, vaccine, adjuvant, immunogenic epitope, luciferase; immunostimulant; cytokine; polyhydroxybutyrate; PHB synthase; body fluid; molecular laser; universal carrier molecule; monomolecular layer.
                                                                                                                                                                                                                                                                                                                                                                Producing S-layer proteins in Gram-negative bacteria or eukaryotes -
integrated into membranes or organelles or secreted into periplasma or
growth medium, and nucleic acid encoding S-layer proteins with peptide
insertions, used in vaccines or for enzymatic reactions.
                                                                                                                                                                         1. .31
/label= signal_peptide
                                                                                                                                                             Location/Qualifiers
Æ
                                                                 B stearothermophilus sbsB protein.
AAW93253 standard; protein; 920
                                                                                                                                           Geobacillus stearothermophilus.
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N-PSDB; AAX22751
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                                    17-0CT-2003
24-AUG-1999
                                                                                                                                                                                                                                          04-FEB-1999,
                                                                                                                                                                        Peptide
                                                                                                                                                                                           Protein
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This invention describes a method for the production of a S-layer protein comprises (a) preparing a Gram-negative prokaryotic host cell transformed with nucleic acid (II) inhocked to a signal sequence (SS) that encodes a protein which causes at least one of (i) into the external or cytoplasmic membranes and/or (ii) secretion of (I) into the periplasmic space or extracellular medium. (b) culturing the call to express (I) and (c) optionally recovering (I) from the membranes, periplasmic call is and/or extracellular medium. (b) culturing the call to express (I) and (c) optionally recovering (I) from the membranes, periplasmic call is used as host and then the SS, which is optional, promotes integration into the extracellular medium. (c) is optional, promotes integration into the extracellular medium. (c) are useful as (i) vaccines or and variety of polypeptide inserts and are useful as (i) vaccines or adjuvants (with immunogenic epitopes or immunostimulants inserts such as cytokines) (ii) as reactors (inserts are enrywes, e.g. polyphydroxybutyrate (PHB) synthase for use as a 'molecular spinnerette' for production of PHB or luciferase for use as a molecular contined with substrate and oxygan) and (iii) as universal carrier molecule (streptavidin is inserted) for use in hybridisation and immuno assays, or for selective elimination of cytokines, toxines tor, from body fluids (inserte are specific binding epitopes). In this system, heterologous [1] do not form inclusion bodies but rather monomolecular layers, and in eukaryotic cells they undergo glycosylation. This sequence represents the Bacillus stearothermophilus sbsB protein which is used to illustrate the method of the invention. (Updated on 17-OCT-2003 to standardise OS field)

Disclosure; Page 23-25; 34pp; German.

Sequence 920 AA,

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48;
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                                                                                                                                                              LVTTFEDLLDHWGEEKANILINLGISVG-TGGKWEPNKSVSRAEAAQFIALTDKKYGKKD 182
                                                                                                                                                                                      147 VKLPFTDVNDTWA-PYVKALYKYBVTKGKTPTSFGAYQNITRGDFAQFVY-----RAV 198
                                                                                                                                                                                                                                                                                                                           EKGNADVEYLNLANHDVKFVANNLDGSPANI -- FEGGEATSTTGKLAVGIKQGDYKVEVQ 347
                                                                                                                                                                                                                                                                                                                                                                               VIKRGGLIVSNIGIITVKNLDIPASAIKNVVFALDADNDGVVNYGSKLSGKDFALNSONL 407
                                                                                                                                                                                                                                                                                                                                                                                                         VILPDGVVLTNTFKVTVTEVPV---QVQNQGFTL-VDN-----LSNA-----PQNT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                    VVGEKASLNKLVATIAGEDKVV-----DPGS-----ISIKSSNHGIISVVNN--- 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 -YITAEA--AGEATLTIKVGDVTK-----DVK-----FKVTTDSRKLVSVKANPDKLQ 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      527 GVNQKTIKVSAV--DQYG-----KEI--KFGT---KGKVTVTTNTEGLVIKAVN- 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SDNTIDFDSGNSATDQFVVVATKDKIVNGKVEVKYFKNASDTTPISTKTITVNVV 623
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                                                                      AGFTDVPKD-RAKYVNALVEAGVLNGKAPGKFGAYDPLTRVENAKIIANRYKLK---ADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVQNKTLPVTFVTTDQYGDPFGANTAAIKEVLPKTGVVAEGGLDVVTTDSGSIGTKTIGV
                                                                                                          PSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGE
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                                                                                                                                                                                                                                                                                              KPFTRNQEYTITATGIKNLKGETAKELTGKFVWSVQDAVTVALNNSSLKVGBESGLTVKD
                                                     SPPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDENAQ
                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 555 TGNDVGEGTVHFQNGATLGSLYV----NVTEGNVAFKNFELVS-----
8.7%; Score 367; DB 2; Length 920;
Larity 23.3%; Pred. No. 4.7e-13;
Conservative 138; Mismatches 369; Indels 240;
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               al Similarity
227; Conserv
  Query Match
Best Local S
Matches 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PN
                                                                                                                              epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                  The isolation and purification of the high molecular weight protein enables the identification of the major protective epitopes of the protein by conventional epitope mapping. These epitopes can then be synthesised using standard techniques and incorporated into fully synthetic or recombinant vaccines. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYGKKDNAQAYVTDVKVSEPTKLTLTGTGLDKLSADDVTLEGDKAVAIEASTDGTSAVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASGGNADAKKVTFDKVKDSKISTDGHNVTLNSEVKTSNGSSNAGNDNSTGLTISAK----
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                                                                                                                                                                                                                                                                                                                                                                         molecular weight surface proteins - of non-typeable haemophilus
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                                                                                                                            high molecular weight protein; virus; vaccine; influenza;
nity; haemophilus influenzae.
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6.1%; Score 257.5; DB 2;
Best Local Similarity 22.0%; Pred. No. 2.1e-06;
Matches 183; Conservative 104; Mismatches 328;
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                                                                                                                                                                                                                                                                                     INST NAT SANTE & RECH MEDICALE
                                                                                                      High molecular weight protein 3 (HMW3)
                                                                                                                                                                                                                                                                                                                                                                                       which exhibit immunogenic properties
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                      1338
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                      AAR41731 standard; protein;
                                                                    (revised)
(first entry)
                                                                                                                                                                 Haemophilus influenzae
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N-PSDB; AAQ49510.
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                                                                    25-MAR-2003
26-APR-1994
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                                                                                                                                              immunity;
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1168 İIKGNITSQNVTVTATENLVTTENAVINA-----TSGTVNISTKTGDIKGGIESTSGN 1220
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                                        This protein comprises the high molecular weight surface protein HMW3 (125 kba) of non-typeable Haemophilus influenzaes strain 5 that has the immunological ability to protect against disease caused by a non-typeable Haemophilus strain and is characterised by at least one surface-exposed Beneficope that is recognised by monoclonal antibody ADG. The HWW3 amino acid sequence was deduced from an isolated hmw3 gene (see AAN30291). HMW1 (see AAW30294) and HMW4 (see AAW30292) have also been identified. A conjugate comprising HWW3 inked to an antigen, hapten or polyaaccharide, and a synthetic peptide of 6-150 amino acids corresponding to at least protective epitope of HWW3 are also claimed. HWW proteins, conjugates and peptides can be used in vaccines, as immunogens for preparation of antibodies and as antigens for detection of these antibodies. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ATAGKATVELVOETIAIKSVNFKPVOTENFVEKKINIGTVLELEKSNLDDIVK-G 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349 TXRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDFALNSQNLV 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GRSDSSEA------ENANLTIQTKEL-KL-AGDLNISGFNKAEITAKNGSDLTIGN
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                                                                                                                                                                                                                                                                                                  DB 2; Length 1598;
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                                                                                                                                                                                                                                                                                                6.1%; Score 257.5; DB 2;
llarity 22.0%; Pred. No. 2.6e-06;
Conservative 104; Mismatches 328;
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               1; Page 93-97; 183pp; English
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les 183; Conserv
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                                                                                                         VNITASGNTLKVSNITGQDVTV-----TADAGALTTTAGSTISATTGNANITTKTGD 1012
                                                                                                                                                            GDIEGTISGNTVNVTASTGDLTIGNSAKVEAKNGAATLTAESGKLTTQ----TGSSI--- 1125
                                                                                                                                                                                                                                                                                                                                                               KLDGAASGDRIVVNAINASG-----SGN---VIAKISSSVNIIGDLNTIN 1222
                                                                                                                                                                                                        562
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             TKRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDFALNSQNLV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-typeable Haemophilus; high molecular weight surface protein; HMW3; immunogen; vaccine; otitis media.
                                                                                                                                                                                                      ------VVAEGGLDVVTTDSGSIGTKTIGVTGNDVGEG
                                                                                                                                                                                                                                                                                                                                  KY----TSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVTGKTPGKVDIH----LTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High molecular weight proteins of non-typeable Haemophilus influenzae useful for vaccine production.
                                          TIKGNITSONVTVTATENLVTTENAVINA------TSGTVNISTKTGDIKGGIESTSGN
                                                                                                                                      VIKDVK-----FVTIDSRKLVSVKANPDKLQVVQNKTLPVT--FVTIDQY
                                                                                                                                                                                                                                                                   TVHFQNGNGATLGSLYVNVTEGNVAFKNFELVSKVGQYGQSPDTKLDLNVST-TVEYQLS
                                                                          VGEKASLNKL-VATIAGEDKVVDPGSISIKSSNHGIISVVNNYITAEAAGEATLTIKVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN------LIKETQHKVRVVKSG---AEQGKLYLDRNGDAVFNAGD 766
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                                                                                                                                                                                                    GDPFGANTAAIKEVLPKTG-
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(first entry)
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14-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --ASTDGT---SAVVTLGGKVAPNKD-----LTVKVKNOSFVTK----FVYEVKKLA 268
                                                                                                                                                                                                                                                                                                                                                            DPGSISIKSSNHGIISVVNNYITAEAAGEATLTIKVGDVTKDVK------FKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             320 FEHDMYVIVDWHVHAPGDPRADVYSGAYDPFEBIADHYKDHPKN---HYIIWELANEP--
                                                                                                                                           FVANNLDGSP--ANIFEGGEATSTTCKLAVGI--KQGDYKVEV---QVTKRGGLTVSNTG
                                                                                                                                                                                                                                                                                                                      491 ANGDGGPYFDEADVWLNFLNKHNISWANWSLTNKNEISGAFTPFELGRIDAT-----DL
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                                                                     OAIAFKLNDEKGNADVEYL - - NLANHDVK
                                                                                                                                                                                --SPNNNGGPGLTNDEKGWEAVKEYAEPIVEMLREKGDNMILVGNPNWSORPDLSADNP-
                                                                                                                                                                                                                                                                                       -----VVNYGSK--LSGKDFALNSQNLVVG--EKASLNKLVATIAGEDKVV
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                                                                                                                                                                                                                   361 IITVKNL-----DIPAS----AIKNVVFALD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      TDS--RKLVSVKANPDKLQV----VQN-----
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1. .584
/note= "claim 2"
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(revised)
(first entry)
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27-AUG-2003
06-FEB-1991
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 1483 GLNIISENGRNTVRLRGKEIDVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The amino acid sequence of the full length alkaline cellulase. The gene encoding the protein was isolated from Bacillus sp. KSM-365 chromosomal DNA and inserted into the E.coli vector BR322. The gene was subsequently used to produce expression vectors contg. a 1071 fragment of the gene covering amino acid residues 228-584 (AAQ94349). The expression vectors contg. the fragment were transformed into B.subtilis for production of the protein. The novel alkaline cellulase has high specific activity in an alkaline environment and is stable over wide ranges of temp. and pit, and has full activity in the presence of surface active agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 PSDVKKTSWSPPYIKDLYEQEVITGTSATTFSPTDSVTRAQFTVMLTRGLGLEASSKDYP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 ---KDKVNGELVTTF-EDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTDKKYGKKDNAQAYVTDVKVSEPTK-----LTLTGTGLDKLSADDVTLEGDKAVAIE- 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLIMKVASHD--YLYHTEA-VKSPSEAGALQLVELNG-----QLTLAGEDGTPVQL 259
                                                                                                                                                                                                                                                                                                              Alkaline cellulase; Bacillus; E.coli; pBR322; expression vector; stable; B.subtilis; specific activity; surface active agent; chelating agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alkaline cellulase and related DNA, vectors and transformed microbes - useful for prodn. of a highly specific enzyme in alkaline environments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNL-----
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                                                              IN------LIKETQHKVRVVKSG---AEQGKLYLDRNGDAVFNAGD 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 941;
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21.3%; Pred. No. 2.6e-06;
ive 109; Mismatches 291;
                                                                                                                                                                                                                                                                           Full length Bacillus sp. alkaline cellulase.
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                                                                                                                                                                AAR77395 standard; protein; 941
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N-PSDB; AAQ94350.
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ee 193; Conserv
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Job time : 68 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SPNNNGGPGLTNDEKGWEAVKEYAEPIVEMLREKGDNMILVGNPNWSQRPDLSADNP- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 -IDAENIMYSVHFYTGSHGASHIGYPEGTPSSERSNVMANVVLLLDNGVAVFATEWGTSQ 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 RGMSTHGLQWFGEIVNENAFVALSNDWGSNMIRLAMYIGENGYATNPEVKDLVXBGIELA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 FVANNLDGSP--ANIFEGGEATSTIGKLAVGI--KQGDYKVEV---QVIKRGGLIVSNTG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPGSISIKSSNHGIISVVNNYITAEAAGEATLTIKVGDVTKDVK-------FKVT 477
                                                                                                                   cellulase gene - originated from alkalophilic Bacillus
                                                                                                                                                                                                                                                                                                                                                        116
                                                                                                                                                                                                                                                                                                                                                                                                                    - FKDRKN-WAYKEIQAAYEAGIVTGKTNGEFAPNENITREQMAAMAVRAYEYLENELSLP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                              ---KDKVNGELVTTF-EDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 LTDKKYGKKDNAQAYVTDVKVSEPTK-----LTLTGTGLDKLSADDVTLEGDKAVAIE- 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 --ASTDGT---SAVVTLGGKVAPNKD-----LLTVKVKNQSFVTK----FVYEVKKLA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 VEKLIF-----,----DDDRAG------QAIAFKLNDEKGNADVEYL--NLANHDVK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 FEHDMYVIVDWHVHAPGDPRADVYSGAYDFFEEIADHYKDHPKN---HYIIWELANEP-- 374
                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                     DNA encoding the sequence can be introduced into E.coli to give a recombinant strain for prodn. of cellulase protein. (Updated on 27-AUG-2003 to correct OS field.) (Updated on 24-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                            SFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IITVKNL-----DIPAS----AIKNVVFALD------
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                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                              Query Match 6.0%; Score 251.5; DB 2; Length 941; Best Local Similarity 21.3%; Pred, No. 2.9e-06; Matches 193; 'Conservative 108; Mismatches 292; Indels 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 TDS--RKLVSVKANPDKLQV----VQN------
                                                                                                                                                           Claim 1; Fig 1; 21pp; Japanese.
88JP-00109545
                        88JP-00109545
                                                                          WPI; 1990-330487/44.
N-PSDB; AAQ06320.
                                                                                                                    segment contg. c codes cellulase.
                                                  (KAOS ) KAO CORP
                                                                                                                                                                                                                                                          Sequence 941 AA;
02-MAY-1988;
                         02-MAY-1988;
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                                                                                                                                                                                                                        720 ATSPEDNTMSNIILFVGTEDADVISLDNITVSGTEIEUVIHDEKGT-ATLPSTFEDGTR
                                                                                                                                                                                           -----GOSPDTKLDLNVSTTVEYQLSKYTSDRVXSDPENLEG
AEGGLD------VVTTDSGSIGTKTIGVTGNDVGEGTVHFQNGNGATLGSLY----
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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	r U		
19 BW Model	April 7, 2004, 17:23:54; Search time 46 Seconds (without alignments) 4755.947 Million cell updates/sec	US-09-844-281-1 4202 1 AGKSFPDVPAGHWAEGSINYITSEIGSQAVHVNVLNNPNL 833	sxt 0.5
om procein - procein search, using sw model	April 7, 2004, 1	US-09-844-281-1 4202 1 AGKSFPDVPAGHWAI	BLOSUM62 Gapop 10.0 , Gapext 0.5
OM protein - pro	Run on:	Title: Perfect score: Sequence:	Scoring table: BLOSUM62 Gapop 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

1071772

Total number of hits satisfying chosen parameters:

1071772 seqs, 262633353 residues

Searched:

/USO7/PCT_N	pubpaa/US06_ pubpaa/US07_ pubpaa/PCTUS pubpaa/US08_	<pre>c./pcocata///puppaa/vole_tuberomb.pep:* 6/pcodata///puppaa/US09A_PUBCOMB.pep:* 6/pcodata/2/pubpaa/US09B_PUBCOMB.pep:* 6/pcodata/2/pubpaa/US09C_PUBCOMB.pep:* 6/pcodata/2/pubpaa/US09C_PUBCOMB.pep:* 6/pcodata/2/pubpaa/US09PWBW PUB.pep:*</pre>	2/pubpaa/US10Ä_PU 2/pubpaa/US10B_PU 2/pubpaa/US10C_PU 2/pubpaa/US10_NEW 2/pubpaa/US60_NEW
Applicati 6/ptodata/ 6/ptodata/ 6/ptodata/	/cgn2_6/ptodata/2/ /cgn2_6/ptodata/2/ /cgn2_6/ptodata/2/ /cgn2_6/ptodata/2/	/cgnz_6/ptodata/z/ /cgnz_6/ptodata/z/ /cgnz_6/ptodata/z/ /cgnz_6/ptodata/z/	6/ptodata 6/ptodata 6/ptodata 6/ptodata 6/ptodata 6/ptodata
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Database			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		οko			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ΩI	Description
! ed !	4202	100.0	833	. 6	US-09-844-281-1	Sequence 1, App]
01	564.5	13.4	529	12	US-10-282-122A-45596	Seguence 45596,
m	556.5	13.2	414	12	US-10-282-122A-45560	Seguence 45560,
4	553.5	13.2	525	12	US-10-282-122A-46674	Sequence 46674,
N	459	10.9	379	12	US-10-282-122A-45308	Seguence 45308,
φ	374	8	1222	თ	US-09-137-531-15	Sequence 15, Apr
7	374	8.9	1252	σ	US-09-137-531-9	Sequence 9, Appl
œ	369	8.8	408	12	US-10-282-122A-46594	Sequence 46594,
σ	367.5	8.7	921	σ	US-09-117-447-6	Sequence 6, Appl
10	257.5	6.1	1599	13	US-10-092-880-9	Sequence 9, Apr
11	249.5	5.0	1600	13	US-10-092-880-10	Sequence 10, Ar
12	249.5	5.9	2353	თ	US-09-797-862-33	Sequence 33, Apr
13	246	5.9	1180	14	US-10-193-764-61	Sequence 61, Ag
14	246	5.9	1188	14	US-10-193-764-59	Sequence 59, Ag
15	242.5	5.8	1220	14	US-10-193-764-28	28,

Sequence 26, Appl	Sequence 53, Appl	Sequence 51, Appl	Sequence 67070, A	Seguence 66695, A	Sequence 304, App	Sequence 32, Appl	Sequence 30, Appl	Sequence 45, Appl	Seguence 43, Appl	Seguence 43144, A	Sequence 4, Appli	4,	'n	'n	4			Sequence 41, Appl				Sequence 2, Appli			ednence	34,	9	Sequence 32, Appl	Sequence 1, Appli
US-10-193-764-26	US-10-193-764-53	US-10-193-764-51	: US-10-282-122A-67070	: US-10-282-122A-66695	US-09-741-669-304	US-10-193-764-32	US-10-193-764-30	US-10-193-764-45	US-10-193-764-43	: US-10-282-122A-43144	US-10-175-282-4	US-10-175-275-4	US-10-175-282-3	US-10-175-275-3	US-10-282-122A-45123	7 15 US-10-369-493-10178	US-09-813-214A-9	US-10-193-764-41	US-10-193-764-39	US-10-282-122A-51483	US-10-193-764-65	US-10-092-880-2	US-10-193-764-63	US-10-282-122A-61210	US-10-193-764-37	US-10-193-764-34	US-10-282-122A-62947	-09-797-862	US-09-841-786-1
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5. 8.	5.6	5.6	5.6	5.5	5.5	5.4	5.4	5,4	S.	ω	5.3	ы Э	5.3	5.3	5.3	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.1	5.1	5.1	5.1	5.1	5.0
242.5	235	235	235	230.5	230	229	229	227.5	227.5	223.5	222	222	222	222	222	220.5	218.5	217.5	217.5	217	216.5	216.5	216.5	216	215.5	215.5	214.5	213	211.5
16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	. 45

ALIGNMENTS

RESULT 1	
; Sequence 1, Patent No.	Sequence 1, Application US/09844281 Sequence 1, Application US/09844281 Patent No. US20020082386A1
; GENERAL INFORMATION: : APPLICANT: Mangold;	ORMATION: . Mangold, Beverly L.
, APPLICANT:	Aldrich,
, APPLICANT:	
; TITLE OF INVENTI	TITLE OF INVENTION: Anthrax Specific Antibodies FTLR REFERENCE: 38602.0003
CURRENT A	CURRENT APPLICATION NUMBER: US/09/844,281
CURRENT F	FILING DATE: 2001-04-30
; PRIOR APPI	PRIOR APPLICATION NUMBER: 60/200,505
NUMBER OF	SEO ID NOS: 3
; SOFTWARE:	Patentin version 3.1
; LENGIH: 8	833
, ORGANISM: B US-09-844-281-1	Bacillus anthracis 1-1
Query Match	100.0%;
Matches 8.	Best Local Similarity 100.0%; Fred. No. 1.18-290; Matches 833; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
λō	1 AGKSFPDVPAGHWAEGSINYLVDKGALTGKPDGTYGPTESIDRASAAVIFTKILNLPVDE 60
q	1 AGKSFPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDE 60
Qy 61	NAQPSFKDAKNINSSKYIAAVBKAGVVKGDGKENFYPBGKIDRASFASMLVSAYNLKDKV 120
Db 61	NAQPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKV 120
Qy 121	NGELVITFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGK 180
Db 121	

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294 MEESGSWIRIRVGAGFQWVDKNQLNPVKQE-----NFLEGK-AIIIDPGHGGIDSGNVGY 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NAQPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 --KKYGKKDNAQAY-----VTDVKVSEPTKLTLTGTGLDKLSADDVTLEGDKAVAIE 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 ASTDGTSAVVT-LGGKVAPNKDLTVKVK--NQSFVTKFVYEVKKLAVEKL-TFDD---- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 GIKQGDYKVEVQV-----TKRGGLTVSNTGIITVK-NLDTPASAIKNVVFALDADNDGV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNYGSKLSGKDFALNSQNL-------VVGEKASLNKLVATIAGEDKVVDFGSISIKSSN 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 ORADGWLKIVTSKGEKWTP---LTBKTETINBEFTT---YETASHSSKVLGTYNAQTVTV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 IGELPTQFKDLEPHWGKKQANILVALEISKGTGNGWNPEGTVTRAEAAQFIAMADQNKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 YEKESETVLDVSLRLKKIFEQKAPFTVMFTRTDNTRPGVNSTDSLKKRVEFAQEHNGDIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | : | : | : | : | 408 VSIHANGSAEKNGQGTETLYYQSARAKVTNPHVEDSKLLA----QKIQDRLVAALGTKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 AAKKFSDVPT--WAQQSVDYLVGKKALDGKPDGTFSPSEAVDRGSAAKILAVVLGLPVDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGKSFPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 - DRAGOAIAFKLNDEKGNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATSTTGKLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
13.4%; Score 564.5; DB 12; Length
Best Local Similarity 32.6%; Pred: No. 11e-31.
Matches 172; Conservative 81; Mismatches 192; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 TSKRMYMNRNVITYHQPSLSSGITDVQ-HKPQMVEVT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See File
PRIOR PELICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR PILING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2010-02-06
PRIOR PELING DATE: 2010-02-06
PRIOR PELING DATE: 2010-02-06
PRIOR PELING DATE: 2010-02-06
PRIOR PELING DATE: 2010-02-16
PRIOR PELING DATE: 2010-03-16
PRIOR PELING PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PELING DATE: 2010-03-16
PRIOR PELING DATE: 2010-03-16
PRIOR PELING PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PR
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; Sequence 45560, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bacillus anthracis
US-10-282-122A-45596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 GXTPGKVDIHLTKNGATAGKATVEIVQETIAIKSVNRKPVQTENFVEKKINIGTVLELEK 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  780
                                KDNAQAYVTDVKVSEPTKLTLTGTGLDKLSADDVTLEGDKAVAIEASTDGTSAVVTLGGK 240
                                                                                                                                                                             RKLVSVKANPDKLQVVQNKTLPVTFVTTDQYGDPFGANTAAIKEVLPKTGVVAEGGLDVV 540
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                                                                                                                             VAPNKDLTVKVKNOSFVTKFVYEVKKLAVEKLTFDDDRAGQALAFKLNDEKGNADVEYLN 300
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APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: G0/207,727
PRIOR APPLICATION NUMBER: G0/230,335
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNLDDIVKGINLTKETQHKVRVVKSGAEQGKLYLDRNGDAVFNAGDVKLGDVTVSQTSDS
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
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Yamamoto, Robert
Forsyth, R.
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61 NAQPSFXDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKV 120
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FRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

FRIOR APPLICATION NUMBER: 60/206,848

FRIOR FILING DATE: 2000-05-26

FRIOR FILING DATE: 2000-05-26

FRIOR FILING DATE: 2000-05-26

FRIOR FILING DATE: 2000-05-26

FRIOR FILING DATE: 2000-05-26

FRIOR FILING DATE: 2000-09-06

FRIOR FILING DATE: 2000-09-06

FRIOR FILING DATE: 2000-09-06

FRIOR FILING DATE: 2000-10-23

FRIOR FILING DATE: 2000-11-27

FRIOR FILING DATE: 2000-11-27

FRIOR FILING DATE: 2000-11-27

FRIOR FILING DATE: 2000-12-22

FRIOR FILING DATE: 2000-12-22

FRIOR FILING DATE: 2000-12-22

FRIOR FILING DATE: 2000-12-22

FRIOR FILING DATE: 2001-12-22

FRIOR FILING DATE: 2001-12-22

FRIOR APPLICATION NUMBER: 60/269,308

FRIOR FILING DATE: 2001-02-16

FRIOR FILING DATE: 2001-02-16

FRIOR APPLICATION NUMBER: 60/269,308

FRIOR FILING DATE: 2001-02-16

FRIOR APPLICATION NUMBER: 60/269,308

FRIOR FILING DATE: 2001-02-16

FRIOR APPLICATION NUMBER: 60/269,308

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FRIOR APP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109;
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                                                            -10-282-122A-46674
Sequence 46674, Application US/10282122A
Publication No. US20040029129A1
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LOCATION: (364)...(364)
OTHER INFORMATION: X=any amino acid
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CATTON: (493)...(493)

CHER INFORMATION: X=any amino acid
US-10-282-122A-46674
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Yamamoto, Robert
Forsyth, R.
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                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Samudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Wall, Daniel
Trawick, John
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Best Local Similarity 31.8<sup>§</sup>
Matches 164; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 KDNAQAYVTDV-----KVSEPTKLTL-TGTGLDKLSADDVTLEGDKAVAI--EA 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 STDGTSAVVTLGGKV----APNKDLTVKV-----KNQSFVTKFVYEVKKLAVEKLTFDD 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 GNPGSNKNESLANRVKFGQENNADIFVSIHANSSEKHDGHGTETYYYKKSKRGEETQIEK 322
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FRIOR APPLICATION NUMBER: 60/191,078
FRIOR PILING DATE: 2000-03-21
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR FILING DATE: 2000-05-23
FRIOR APPLICATION NUMBER: 60/206,727
FRIOR APPLICATION NUMBER: 60/230,335
FRIOR APPLICATION NUMBER: 60/230,347
FRIOR APPLICATION NUMBER: 60/230,347
FRIOR APPLICATION NUMBER: 60/230,347
FRIOR PILING DATE: 2000-09-09
FRIOR PILING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR PILING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-16
FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-16
FRIOR PILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-06
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FRIOR FILING DATE: 2000-02-07
FRIOR FILING DATE: 2001-02-06
FRIOR FILING DATE: 2001-02-06
FRIOR FILING DATE: 
                                                                                                                                                                                                                                                                                                                       APPLICANT: Xù, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA-034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
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13.2%; Score 556.5; DB 12; Length
Best Local Similarity 39.2%; Pred. No. 2.9e-31;
Matches 145; Conservative 54; Mismatches 120; Indels
                                    Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-45560
Judith
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376 NGKLATESGR 385
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82 SPKDSQNHWGTPYMPAAEKAGSIKVEGKGIFNPSGKVTRAAMATMLVNAYKLQNKNTSNG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 KDLIVKVKNOSFVIKFVYEVKKLAVEKLI------FDDDRAGQAIAFKLNDEKGNADV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 KD-TKGLPXKXIVLDTSLRLQKL-LEKHTPFTVLLNSXSDTRTGHGSKSSL-QERG--- 272
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273 KFAKTKQGDILIMGH-----ANAFNGNGKRTETYYXXSSKSEKTNPHVEKKPGFPGKIQ 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 SFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGEL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 VITFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGKKDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 FPDVPA--WADKSVTYLVDKQVLSGYPDGTFGSSDTLDRASAATIMTTALGIHIDLNAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 FPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDENAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 OSKFEEFKGHWGGKIPNTLIGFEISVGTDNGWOPNKFITRAEAAQLTAKTD----
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US-09-137-531-15

Sequence 15, Application US/09137531

Patent No. US20020046816A1

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Expression of surface layer proteins
NUMBER OF SEQUENCES: 25

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
10.9%; Score 459; DB 12; Length 3'
Best Local Similarity 32.5%; Pred. No. 2.2e-24;
Matches 124; Conservative 49; Mismatches 110; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: X=any amino acid US-10-282-122A-45308
                                                                                                                                                                                                   LOCATION: (227)..(227)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (304)...(304)
OTHER INFORMATION: X=any amino acid
FEATURE:
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SOFTWARE: Patentin version 3.1
                                                                                                               ORGANISM: Bacillus anthracis
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC FEATURE
LOCATION: (255)..(255)
OTHER INFORMATION: X=any
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OTHER INFORMATION: X=any
                                                                                                                                     FEATURE:
NAME/KEY: MISC FEATURE
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NAME/KEY: MISC FEATURE
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APPLICANT: TOUSYLING.
ITILE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 014
CURRENT APPLICATION NUMBER: 04/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-09
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PRIOR PILING DATE: 2001-02-16
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                        NGELVITFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGK 180
                                                              | | : : | | : : | | : : | | : : | | 401 GDIFVSIHANGSAEKNGQGTETLYYQSARAKVTNPHVEDSKLLAQKIS-DRLVAALGTKD 459
                                                                                                                                     181 KDNAQAY------VTTDV-----KVSEPTKLTLTGTGLDKLSA----- 211
                                                                                                                                                                                          198 STSKRMYMTRNVITYHHPSLSSGITDVHHKPQNGKVTEQ-----RADGWVKMLTSKREKW 252
                                                                                                                                                                                                                                                     212 DDVTLEGDKAVAIEASTDGTSAVVTLGGKVAPNKDLTVKVKNQSFVTKFVYEVKKLAVEK 271
                                                                                                                                                                                                                                                                                                             -----ASHSSKVLGTYNAQTVTVMBKEWXLIRI-- 300
                                                                                                                                                                                                                                                                                                                                                                    272 LTFDDDRAGQAIAFKLNDEKGNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATSTTG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 KLAVGIKQGDYKVEVQ-----VTKRGGLTVSNTGIITVK-NLDTPASAIKNVVFALDAD 384
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NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Mandone, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John
APPLICANT: Tawick, John
APPLICANT: Garr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
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72 IWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGELVTTFEDL 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLGGK------VAPNKDLTVKVKNQSFVTKFVYBVKKLAVEKLTFDDDRAGQAIAF 285
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                                                                                                                                                                                                               :: | : | : | : | : | : | ---AWEALLTOYATEGOKUTISYNV--DGDTUT 864
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                      ---SYTGVA 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 VKAINNTTVEVTFEEEVTNVQALNFKIEGLEIKNASVKQTNKKVVVLTTEAQTADKEYVL
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                                                                                                                                                                                   DAVFNAGDVKLGDVTVSQTSDSALPNFKADLYDTLTTKYTDKG---TLVFKVLKDKDVIT
                                                                            702 TE-NFVEKKINIGTVLELEKSNLDDIVKGINLTKETQHKVRVVKSGAEQGKL--YLDRNG
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8.9%; Score 374; DB 9; Length 1252;
Best Local Similarity 23.3%; Pred. No. 1.6e-17;
Matches 224; Conservative 130; Mismatches 345; Indels 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: FORM:

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PALENTIN Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION NUMBER: US/09/137,531

FILING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION

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; Patent No. US20020048816A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
                                                                                                                       790 TQFNTADSGSNSNSIWFAGKN
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SEQUENCE CHARACTERISTICS:
LENGTH: 1252 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                830 NEVFGEA-
                                                                                                                                                                                                                                                                                         816 SEI 818
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865 FKV 867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 KFKVTTDSR-----KLVSVKANPDKLQVVQNKTLPVTFVTTDQYGDPFGANTAAIKEV 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LDHWGEEKANILINLGISVGT-GGKWEPNKSVSRAE-AAQFIALTDKKYGKKDNAQAY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V----TDVKVS---EPTKLTLTGTGLDKLSADDVTL-EGDKAVAI---EASTDGTSAVV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 TLGGK-----VAPNKDLTVKVKNQSFVTKFVYEVKKLAVEKLTFDDDRAGQALAF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 TLDGETIGGFKGVAAVVPTK---VELVSSAVQGKLGQEVKVQAKVTVAEGQSKAGIPVTF 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 TVPGNNNDGVVPTLTGEALTNEEGIATYSYTRYKEGTDEVTAYATGDRSKFSLGYVFWGV 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNVVFALDADNDGVVNYGSKLSGKDFALNSQNLVVGEKASLNKLVATIAGEDKVVDPGSI 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   526 LPKTGVVAEGG----LDVVTTDSGS----IGTKT------IGVTGNDVGEGTV--- 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 IWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGELVTTFEDL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 ------NULDGSPANIFEGG 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 WAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIPTKILNLPVDENAQPSFKDAK-N 71
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al Similarity 23.3%; Pred. No. 1.5e-17;
224; Conservative 130; Mismatches 345; Indels 264;
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CURRENT APPLICATION DATA:
                                                                                                                                                         08/682,517
                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1222 amino acids
                                             APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06
FILING DATE:
                                                                                                                                                                                                                                                                                      ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-137-531-15
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Best Local S:
Matches 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 NTGIITVXONLDTPASAIKN-VVFALDADNDGVVNYGSKLSGKDFALNSQNLVVGEKASLN 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 OPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ELVTTFEDLLDH-WGEEKANIL-INLGISVGTGGKWEPNKS-VSRAEAAOFIALTDKKY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 GKVAPNKDLTVKVKNQSFVTKFVYBVKKLAVBKLTFDDDRAGQAIAFKLNDEKGN-ADVE 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 YLNLANHDVKFVANNLDGSPANIFEGGEATSTTGKLAVGIKQGDYKVEVQVTKRGGLTVS 357
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                                              PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR PAPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: Patentin version 3.1

LENGTH: 408
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8.8%; Score 369; DB 12; 1
Best Local Similarity 31.0%; Pred. No. 6.5e-18;
Matches 148; Conservative 57; Mismatches 172;
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OTHER INFORMATION: X=any amino acid
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OTHER INFORMATION: X=any amino acid
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OTHER INFORMATION: X=any amino acid
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; OTHER INFORMATION: X=any amino acid
US-10-282-122A-46594
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LOCATION: (184)..(184)
OTHER INFORMATION: X=any
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STHER INFORMATION: X=any
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NAME/KEY: MISC FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    820 TOFNTADSGSNSNSIWFAGKN--------PVKYAGVSGKTYKYFGANG 859
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394 DTILSVEEVTTGASVNNGANKTYKVTYKNPKTGKPEANKTFNVGFVENMNVTSDKVANAT 453
                                                                                         ---AAGEATLTIKV-----GDV----TKDV 472
                                                                                                                                                                                           KFKVTTDSR-----KLVSVKANPDKLQVVQNKTLPVTFVTTDQYGDPFGANTAAIKEV 525
                                                                                                                                                                                                                                                                                                                                                                           526 LPKTGVVAEGG----LDVVTTDSGS----IGTKT------IGVTGNDVGEGTV--- 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 -----HFQ----NGNG----ATLGSLYVNVTEGNVAFKNFELVSKVGQ----- 599
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                                                 375 KNVVFALDADNDGVVNYGSKLSGKDFALNSQNLVVGEKASLNKLVATIAGEDKVVDPGSI 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        646 AVADAKIVGNKVVVTG---KTPGKVDIHLTKNGATAG-KATVEIVQETIAIKSVNFKPVQ 701
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                    555 EYKVIVKDKAGNLAKNEIVNVAFNEDKDRVISTVT-NAKFVDTD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 46594, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
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APPLICATION NUMBER: 60/206,848
                                                                                                                                                           435 SIKSSNHGIISVVNNYITAE----
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APPLICANT: Asmudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Chisen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Panamoto, Robert
APPLICANT: Forsyth, R.
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895 FKV 897
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QY 446 VVNNYITAEAAGEATLTIKVGDVTKDVKFKVTTDSRKLVSVK 487 Db 461 AAINGSELLYTANAGSGKASFEVTLKDNTKRTFTVDVKKDFVLQDIKVDATSVKLSDEA 520 QY 488 ANPDKLQVVQNKTLEVYTTDQYGDFFGANTAAIKEVLPKTGVVAEGGLDVYTDDSGS 1 547 Db 521 VGGGFVEGVNQKTLEVYTKVSAVDQYGKETKFGTKGKVTVTNTFGL 563	OY 548 GTKTIGVTGNDVGEGTVHFONGATLGSLYVNVTEGNVAFKNFELVSKVGQYGQSPDTK 607	RESULT 10 US-10-092-880-9 ; Sequence 9, Application US/10092880 ; Publication No. US20020164354A1 ; GENERAL INFORMATION: ; APPLICANT: Barenkamp, Stephen J. ; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS OF NON-TYPEABLE ; TITLE OF INVENTION: HAEMOPHILUS ; FILE REFERENCE:	CURRENT APPLICATION NUMBER: US/10/092,880 CURRENT FILING DATE: 2002-03-08 FRIOR APPLICATION NUMBER: 09/155,614 FRIOR FILING DATE: 1998-09-09 FRIOR FILING DATE: 1996-04-01 FRIOR PAPLICATION NUMBER: 08/617,697 FRIOR FILING DATE: 1996-04-01 FRIOR APPLICATION NUMBER: FCT/US97/04707 FRIOR FILING DATE: 1997-04-01 SOFTWARE: PALCHIN Ver. 2.1 SOFTWARE: PALCHIN Ver. 2.1	 LENGTH: 1599 TYPE: RT ORGANISM: Haemophilus influenzae US-10-092-880-9 Query Match Est Local Similarity 22.0%; Pred. No. 4.6e-09; Matches 183; Conservative 104; Mismatches 328; Indels 215; Gaps 38; 	YLVDKGAITGKPDGTYGPTESIDRASAAVIFTKII
	RESULT 9 US-09-117-447-6 Sequence 6, Application US/09117447 Sequence 6, Application US/09117447 Sequence 6, Application US/09117447 GENERAL INFORMATION: APPLICANT: SLETTE, Uwe APPLICANT: KUUDEN APPLICANT: KUUDEN APPLICANT: HOWORKA, Stefan APPLICANT: RESCH, Stepanka APPLICANT: RESCH, Stepanka APPLICANT: RESCH, Stepanka APPLICANT: SARA, Margit TILLE OF INVENTION: RECOMBINANT EXPRESSION OF S-LAYER PROTEINS TILLE OF INVENTION WUMBER: US/08/117,447 CURRENT APPLICATION NUMBER: US/08/117,447 PRIOR FILING DATE: 1997-01-31 PRIOR APPLICATION NUMBER: DE/196 03 649.6	Patentin Ver. 2.1 Patentin Ver. 2.1 21 Bacillus stearothern -6	Best Local S Matches 220 Matches 333 64	124 LVTTFEDLLDHWGEBKANILINLGISVGTGGKWEPNKSVSRAEAQFIALTD 147 VKLPFTDVNDTWAPYVKALYKYEVTKLKHQQASVHTKNITLRDFAGFVY 176 KKYGKKDNAQAYVTDVKVSEPTKLTLTGTGLDKLSADDVT-LEGDKAVAIEASTDGT 197RAVNINAVPEIVEVTAVNSTTVKVTFNTQIADVDFTNFAIDNGLTVTKATLSRDKK	OY 232 SAVYILGGKVAPNKDLIVKVKNOSFVTKEVYEVKLAVEKLIFDDDBAGGA 282 Db 253 SVEVYNKPFTRNGEYITIATGIRNLKGETAKELIGKFVWSVODAVTVALNNSSLKVGEE 312 QY 283 IAFKLNDEKGNADVEYLNLANHDVKFVANNLDGSPANIFEGGEATSTTGKLAVGIKGG 340 Db 313 SGLTVKDQDGKDVVGAKVELTSSNITNIVVVSSGEVSVSAAKV-TAVKPG 360 QY 341 DYKVEVQVTKRGGLTVSNITGITTVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDF 400 351 TADVTAKVTLPDGVVLTNTFKVTVTEVPVQVQNGGFTL-VDNLSNA 405 QY 401 ALNSQNLVAPENKAEKVTSMFAGETKTVAMYDTKNGDPETKPVDFKDATVRSLNPIIAT 460

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Publication No. US2002164334A1

GENERAL INFORMATION:

APPLICANT: BERENCAMP, Stephen J.

TITLE OF INVENTION: HAEMOPHILUS

FILE REPERENCE

CURRENT APPLICATION NUMBER: US/10/092,880

CURRENT APPLICATION NUMBER: US/10/092,880

FILE REPERENCE:

CURRENT APPLICATION NUMBER: 09/155,614

PRIOR FILING DATE: 1998-09-30

FRIOR FILING DATE: 1998-09-30

FRIOR FILING DATE: 1998-04-01

FRIOR FILING DATE: 1997-04-01

FRIOR APPLICATION NUMBER: PCT/US97/04707

FRIOR FILING DATE: 1997-04-01

NUMBER OF SEQ ID NOS: 11

SEQ ID NO 10

LENGTH: 1600

LENGTH: 1600
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                                                      067 ASGGNADAKKVIPDKVKDSKISTDGHNVTLNSEVKTSNGSSNAGNDNSTGLTISAK--- 1122
                                                                                                                                                                                                                                                                 .221 VNITASGNTLKVSNITGODVTV-----TADAĞALTTTAGSTISATTGNANITTKTGD 1272
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   --- KFVYEVKKLAVEKLTFDDDRAGQAIAFKLNDE
                                                                                                                                                                   ----DV---TVNNNVTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAQNG-----
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ilarity 22.2%; Pred. No. 1.7e-08;
Conservative 121; Mismatches 346;
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850 GNIN-ITNKANVTLQADTSNSNTGLKKRTLTLGNISVEGNLSLTGANANIVGN--LSIAE 906
                                                                                                    DENAQPSFKDAKNI ---WSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYN
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APPLICANT: PEAK, IAN RICHAED ANSELM
APPLICANT: DENNINGS, MICHAEL PAUL
APPLICANT: DENNINGS, MICHAEL PAUL
TILLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0134
CURRENT APPLICATION NUMBER: US/09/797, 862
CURRENT FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR PILING DATE: 1997-12-12
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                                                                                                                                                                       APPLICANT: Loosmore, Sheena M. APPLICANT: Loosmore, Sheena M. APPLICANT: Yang, Yan-Ping APPLICANT: Yang, Yan-Ping APPLICANT: Xang, Yan-Ping APPLICANT: Rielin, Michel H. TITLE OF INVENTION: MOLECULAR WEIGHT PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH FILE REPERENCE: 1038-1239MIS '104/10/193,764 CURRENT APPLICATION NUMBER: 08/16/193,764 PRIOR PILING DATE: 2002-07-12 PRIOR PILING DATE: 1998-10-07 NUMBER: 09/167,568 PRIOR FILING DATE: 1998-10-07 SOFTWARE: PALENT OF SEQ ID NOS: 91 SOFTWARE: PALENT OF SEQ ID NOS: 91 SOFTWARE: PALENT OF SEQ ID NO 6:1
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5.9%; Score 246; DB 14;
Best Local Similarity 20.2%; Pred. No. 1.9e-08;
Matches 185; Conservative 124; Mismatches 335;
Sequence 61, Application US/10193764 Publication No. US20030133943A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-193-764-61
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: : :	Qy 410	Qy 434 ISIKSSNHGIISVVNNYITAERAGEATLTIKVGDVTKDVKFK 475 11	Qy 476VTIDSRKLVSVKANPDKLQVVQNKTLPVTFVTIDQYGDFFGANTAAIK 523	Qy 524		616 VEYQLSKYTSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVVTGKTPGKVDIHLTKNG	676 ATAGKATVEIVQETIAIKSVNFKEVQTENFVEKKINIGTVLELEKSNLEDIVKGINLTKE	OY 736 TQHKVRVVKSGAEQGKLYLDRNGDAVFNAGDVKLGDVTVSQTSDSALPNFKADLY 790 DD 1005 TTGALTTVKGSSINANSGTLVINAKDAELNGEASGNHTVVNATNANGSGSVI 1056	791 DTLTTKYTDKGTLV	Db 1057 ATTSSRVNITGDLI 1070	RESULT 15 US-10-193-764-28 ; Sequence 28, Application US/10193764	GENERAL INPORMATION: APPLICANT: Loosmore, Sheena M. APPLICANT: Loosmore, Ping APPLICANT: Yang, Yan-Ping	APPLICANT: ALCHEI, MICHEL H. TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS FILE REFERENCE: 1038-1239MIS			Haemophilus influenzae 28	Query Match 5.8%; Score 242.5; DB 14; Length 1220; Best Local Similarity 21.5%; Pred. No. 3.6e-08; Matches 210; Conservative 138; Mismatches 368; Indels 259; Gaps 52;	QY 2 GKSFPDVPAGHWAEGS-INYLVDKGAITGKPDGTYGFTESIDRASAAVIFTKIINLPVDE 60	
OY 559 VGEGTVHFONGN-GATLGSLYVNVTEGNVAFKOFELVSKVGQXGQSPDTKLDLAVSTT 615 Db 873QSGNIGGMISGGKVEVSATKDLITKSGSEIKATAGEVAVTSA 914	616 VEYQLSKYTSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVVTGKTPGKVDIHLTKNG 67	915 T	DD 946 AIGGARILIAISGKLITKASSSIISANBSAKDGSIGGNINAANVILN 996 Qy 736 TCHKVRVVKSGAEQGKLYLDRNGDAVFNAGDVKLGDVIVSQISDSALPNFKADLY 790	Db 997 TIGALTTÜKGSSINANSGTLÜINÄKDAELNGEASGNHTÜNNATNANGSGSVI 1048 Qy 791 DILTTKYIDKGTLV 804	Db 1049 ATTSSRVNITGDLI 1062 PESTETE 14	US-10-193-764-59 ; Sequence 59, Application US/10193764 ; Publication No. US20030133943A1	APPLICANT: LOSSMOLE, Sheena M. APPLICANT: LOSSMOLE, Sheena M. APPLICANT: Yang, Yan-Ping APPLICANT: Xlein, Michel H. APPLICANT: Klein, Michel H. TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH	; TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS ; FILE REFERENCE: 1038-1239MIS ; CURRENT APPLICATION NUMBER: US/10/193,764 ; CURRENT FILING DATE: 2002-07-12	PRIOR APPLICATION NUMBER: 09/167,568 PRIOR FILING DATE: 1998-10-07	SOFTWARE: Patentin Ver. 2.1) IENGTH: 1188 TYPE: PRT CRGANISM: Haemophilus influenzae US-10-193-764-59	Query Match 5.9%; Score 246; DB 14; Length 1188; Best Local Similarity 20.2%; Pred. No. 1.9e-08; Matches 185; Conservative 124; Mismatches 335; Indels 270; Gaps 41;	QY 48_VIFTKILNLPVDENAQPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKID 102	Qy 103 RASFASMLVSAYNLKDKVNGELVTTFEDLLDHWGEEKANILINLGISV-GTGGKWEPNKS 161	Qy 162 VSRAEAAQFIALTDKKYGKKDNAQAYVTDVKVSEPTKLTLTGTGLDK 208 : :	Qy 209 LSADDVTLEGDKAVALEASTDGTSAVVTLGGKVAPNKDLTVKVRNQSFVTKFVYSVKKLA 268 1	OY 269 VEKLTFDDDRAGGAIAFKLNDEKGNADVEYINLANHDVKFVANNLDGSPA 318 Db 492NNKANAL :: : :	319 NIFEGGEATSTTGKLAVGIKQGDYKVEVQVTKRGGLTVSNTGIITVK 36	QY 366NLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDFALNSQNLVV 409

Search completed: April 7, 2004, 17:30:49 Job time : 50 secs

5821, Ap 4, Appli 4, Appli 3, Appli 3, Appli 5434, Ap

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72 IWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGELVTTFEDL 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KINDEKGNADVEYINLANHDVKFVA----NNLDGSPANIFEGG 324
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8.9%; Score 374; DB 2; Length 1222;
Best Local Similarity 23.3%; Pred. No. 2.7e-19;
Matches 224; Conservative 130; Mismatches 345; Indels 264; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 TLDGETIGGFKGVAAVVPTK---VELVSSAVQGKLGQEVKVQAKVTVAEGQSKAGIPVTF
                                                                                                                                                                                                                                                                                                                                                                         surface layer proteins
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US-08-682-517-15
Squence 15, Application US/08682517
Patent No. 5874267
GENERAL INFORMATION:
PAPPLICANT:
TITLE OF INVENTION: Expression of surf
NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MUNDIUM TYPE: Floppy disk'
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 1222 amino acids
TOPOLOGY: linear; MOLECULE TYPE: protein US-08-682-517-15
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(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                               protein search, using sw model
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seq length: 200000000
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 TVPGNNNDGVVPTLTGEALTNEEGIATYSYTRYKEGTDEVTAYATGDRSKFSLGYVFWGV 363
                                               DIILSVEEVTIGASVNNGANKTYKVTYKNPKTGKPEANKTFNVGFVENMNVTSDKVANAT 423
                                                                                                                     SIKSSNHGIISVVNNYITAE----TKDV 472
                                                                                                                                                                                                        LPKTGVVAEGG----LDVVTTDSGS----IGTKT------IGVTGNDVGEGTV--- 564
                                                                                                                                                                                                                                                                        EPKAVAPISYFOAPYLDGSAIKAYKKSDLNKAVTKFDGSETAVFAAELVNOSGKKVTGTS 686
                                                                                                                                                                                                                                                                                              -----YGQ-SPDIKLDLNV----STIVEYQLSKYTSDRVYSDPENLEGYEVESKNL 645
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                                                                          KNVVFALDADNDGVVNYGSKLSGKDFALNSQNLVVGEKASLNKLVATIAGEDKVVDPGSI 434
                                                                                                                                        DLHSTNN----STSNKKYSASALQTTASKVTFAALQAEYTIELTRADNAGEVAAIGATNGR 524
                                                                                                                                                                                                                       VNGVKALQLSN-----GTALDAAQITTDSK------GEATFTVSGTNAAVTPVVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Expression of surface layer protein under OF SUCCENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk computer: IBM PC compatible COPERATING SYSTEM: PC-DOS/NS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DETA:
APPLICATION NUMBER: US/08/682,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-08-682-517-9
'Sequence 9, Application US/08682517
', Patent No. 5874267
', Patent No. 5874267
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CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1252 amino acids
TYPE: amino acid
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; MOLECULE TYPE: protein
US-08-682-517-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            598 -PDTAVYFTGDKAKQISVKTNDKGEATFVIGSDTVNDYATPIAWIDINTSDAKQGDLDEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -------KINDEKGNADVEYLNLANHDVKFVA----NNLDGSPANIFEGG
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                                                                                                 13 WAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDENAQPSFKDAK-N
                                                                                                                                                                                             72 IWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGELVTTFEDL
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                                                  264;
Length 1252;
                                                  Indels
                                                  345;
cch 8.9%; Score 374; DB 2; al Similarity 23.3%; Pred. No. 2.8e-19; 224; Conservative 130; Mismatches 345
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RECOMBINANT POLYPEPTIDES IN HOST CELLS
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853
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                                                                                                     644 NLAVADAKIVGNK--VVVTGK-------TPGKVDIHLTKNGAT-----AGK
                                                                                                                                                              677 KVTPTATTLVGTNDYVEVNGNVLQFKGNDELTLTSSSTVNVDVTADGITKRIPVKYINS
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                                                                                                                                                                                                                                                 ATVEIVOETIAIKSVNFKPVOTEN---FVEKKINIGTVLELEKSNLDDIVKGINLTKETO
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8.6%; Score 362.5; DB 4;
Best Local Similarity 23.3%; Pred. No. 1.3e-18;
Matches 229; Conservative 135; Mismatches 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPARTMENTALIZATION OF REC
FILE REPERENCE: 100564-00070
FILE REPERENCE: 100564-00070
CURRENT APPLICATION NUMBER: US/09/889,572
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: PCT/BP00/00686
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: DE 199 03 345.5
PRIOR APPLICATION NUMBER: DE 199 03 345.5
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-889-572-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09889572
Patent No. 6610517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 903 DDNNLLAAPVSVNV 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                814 ITSEIGSQAVHVNV 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-889-572-4
                                                                                                                                                                                                                                                 681
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                                                        Sequence 6, Application US/09463402

Sequence 6, Application US/09463402

Patent No. 6596510

GENERAL INFORMATION:
APPLICANT: Lubitz, Werner
APPLICANT: Resch, Stephanie
TITLE OF INVENTION: and into the Extracellular Space
FILE REFERENCE: 05649059
CURRENT APPLICATION NUMBER: US/09/463,402
CURRENT PILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: DE19732829.6
PRIOR FILING DATE: 1997-07-30
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 6
LENGTH: 920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVNGE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVTTFEDLLDHWGEEKANILINLGISVG-TGGKWEPNKSVSRAEAAQFIALTDKKYGKKD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAQAYVTDVKVSEPTKLTLTGTGLDKLSADDVT-LEGDKAVAIEAST---DGTSAVVTLG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 GKVAPNKDLTVK---VKN----QSFVTKFVYEVYKLAVEKLTFDDDRAGQAIAFKLND 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 EKGNADVEYLNLANHDVKFVANNLDGSPANI--FEGGEATSTTGKLAVGIKQGDYKVEVQ 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ODGK-------DVVGAKVELTSSNTNIVVVSSGBVSVSAAKV-TAVKPGTADVTAK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 VTKRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDFALNSQNL 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 VVGEKASLNKLVATIAGEDKVV-----DPGS-----ISIKSSNHGIISVVNN--- 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 LLVTANAGOSGKASFEVTFKÖNŤKRTFTVĎVKKDPVLQDIKVDATSVKĽSDEAVGGGEVE 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVQNKTLPVTFVTTDQYGDPFGANTAAIKEVLPKTGVVAEGGLDVVTTDSGSIGTKTIGV 554
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llarity 23.3%; Pred, No. 5.8e-19;
Conservative 138; Mismatches 369; Indels 240;
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Best Local Similarity
Matches 227; Conserv
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US-09-463-402-6
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                                                                                                                                                                                                                                                                                        564 VIKNVN-----SDNTIDFDSGNSATDQFVVVATKDKIVNGKVEVKYFKNASDTTPTSTK 617
                                                                                                                                                                                                                                                                                                                                  -----KVGQYGQSPDTKLDLNVSTTVEYQLSKYTSDRVYSDPENLEGYBVE 641
                                                                                                                                                                                                                                                                                                                                                    S----KNLAVADAKIVGNK--VVVTGK--------FPGKVDIHLTKNGAT--- 677
                               361 TADVTAKVTLPDGVVLTNTFKVTVTEVPV---QVQNQGFTL-VDN-----LSNA-- 405
                                                                 401 ALNSQNLVVGEKASLNKLVATIAGEDKVV-----DPGS------ISIKSSNHGIIS 445
                                                                                                                               446 WWW----YITAEA--AGEATLTIKVGDVTK-----DVK-----FKVTTDSRKLVSVK 487
                                                                                                                                                               461 AAINGSELLVTANAGOSGKASFEVTPKONTKRTFTVDVKKOPVLQDIKVDATSVKLSDEA 520
                                                                                                                                                                                                 488 ANPDKLQVVQNKTLPVTFVTTDQYGDPFGANTAAIKEVLPKTGVVAEGGLDVVTTDSGSI 547
                                                                                                                                                                                                                               521 VGGGEVEGVNQKTIKVSAV--DOYG------KEI--KFGT---KGKVTVTTINTEGL 563
341 DYKVEVQVTXRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDF 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AGKATVEIVOETIAIKSVNFKPVOTEN---FVEKKINIGTVLELEKSNLDDIVKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  731 PVKYINSASVP-ASATVATSPVTVKLNSSDNDLTFEELIFGVIDPTQLVKD--EDINEFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KVRVVKSGAE------GGKLYLDRN-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  788 AVSKAAKNDGYLYNKPLVTVKDASGKVIPTGANVYGLNHDATNGNIWFDEEQAGLAKKFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAVEN-----AGDVKLGDVTVSQTSDSALPNFKADLYDTLTTKYTDKG-----TLVFK--
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Fatent No. 5928651

GENERAL INFORMATION:
TILLE OF INVENTION:
TILLE OF INVENTION:
TILLE OF INVENTION:
TILLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Virginia
STREET: Virginia
CITY: Arlhigton
STREET: Virginia
COUNTRY: U.S.A.
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COMPUTER: IBM PC compatible
ERSATING SYSTEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/728,470
FILING DATE:
FLISH APPLICATION: 424
PRIOR APPLICATION DATE:
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MEDIUM TYPE: Floppy
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                                                                                                               US PCT/US93/02166
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                                                                                                         APPLICATION NUMBER: US PCT/US93/02:
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATORING APPLE: 16-MAR-1992
ATORING ABORT INFORMATION:
ATOME: BETKETESSET, JETTY W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDPFGANTAAIKEVLPKTG-
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FILING DATE: 16-MAR-1
PRIOR APPLICATION DATA:
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1222 Qy 117 KDKVNGELVTTFEDLLDHWGEEKANJLINLGISVGTGGKWEPNKSVSRAEAAQFIALTDK 17	729 Db 731 SQK-EGNLTISSDKVNITNQITIXAGVEG75	1282 Qy 177 KYGKKDNAQAYUTDVKUSEPIKLILIGGEBKLSADDVTLEGDKAVALEASTDGTSAVVT 236	Db 759GRSDSSEABNANLTIQTKEL-KL-AGDLNISGFNKAEITAKNGSDLTIGN 806	Qy 237 LGGKVAPNKDLTV-KVKNQSFVTKFVYSVKKLAVEKLTFDDDRAGQAIAFKLNDE 290	Db 807 ASGGNADAKKVIFDKVKDSKISTDGHNVTLNSEVKTSNGSSNAGNDNSTGLTISAK 862	QY 291 KGNADVEYLALANHDVKFVANNLDGSPANIFEGGEATSTTGKLAVGIKQGDYKVEVQV 348	Db 863DVTUNNNVTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAQNG 907	349 TKRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDFALNSQNLV	908 TIKGNITSQNVIVIATENLVITENAVINATSGTVNISTKIGDIKGGLESISGN	OY 409 VGECASLNYL-VATIAGEDKVVDPGSISIKSSNHGTISVVNNYITAEAAGETILIKVGD 46/7	468 VIKDVKFKVTIDSRKLVSVKANPDKLQVVQNKTLPVTFVTIDQY	Db 1013 INGKVESSSGSVTLVATGATLAVGNISGNTVTITADSGKLTSTVGSTINGTNSVTTSSQS 1072	Oy . 512 GDPFGANTAAIKEVLPKTGVVAEGGLDVVTTDSGSIGTKTIGVTGNDVGEG 562	1073 GDIEGTISGNTVNVTASTGDLTIGNSAKVEAKNGAATLITAESGKLTTQTGSSI	Qy 563 TVHFQNGNGATLGSLYVNVTEGNVAFKNFELVSKVGQYGQSPDTKLDLNVST-TVEYQLS 621	Db 1126TSSNGQTTLTAXDSSIAGNINAANVTL-NTTGTLTTTGDSKINATSGTLTINAKDA 11	Qy 622 KYTSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVYTGKTPGKVDIHLTKN 674	Db 1181 KLDGAASGDRTVVNATNASGSGNVTAKTSSSVNITGDLNTIN 122	Cy 675 GATAGKATVBIVQBTIAIKSVNFKPVQTENFVEKKINIGTVLELEKSNLDDIVK-G 72	Db 1223 GLNIISENGRNTVRLRGKEIDVKYIQPGVASVEFVIEAKRVLEKVKDLSDEERETLAKLG 1282	Qy 730 INLTKETQHKVRVKSGAEQGKLYLDRNGDAVFNAGD 766	Db 1283 VSAVRFVEPNNAITVNTQNEFTTKPSSQVTISEGKACFSSGN 1324	RESULT 7	S-08-617-697-9; Sequence 9. Application US/08617697 - Datent No. 5977336	GENERAL NO. 257/330 GENERAL THORMATION: STEPHEN J	NVENTION: High Molec NVENTION: of No. 597	QUENCES: 11 CE ADDRESS: Showshow and Watta	; ADDRESSEE: Shoemaker and Mattare, Ltd.; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza; STREET: Bdg. 1	6	56 ZIP: 22202-0286	; COMPOIER READABL	
KLDGAASGDRTVVNATNASGSGNVTAKTSSSVNITGDLNTIN	GATAGKATVEIVQETIAIKSVNFKPVQTENFVEKKINIGTVLELEKSNLDDIVK-G	GINIISENGRNTVRLRGKEIDVKYIQPGVASVEEVIEAKRVLEKVKDLSDEBRETLAKLG	730 INLIKETQHKVRVVKSGAEQGKLYLDRNGDAVFNAGD 766	1283 VSAVRFVEPNNAÍTVATÓNEFTTKPSSQVTISEGKACFSSGN 1324		US-08-719-641-9 ; Sequence 9. Application US/08719641	Patent No. 6218141 GENERAL INFORMATION	APPLICANT: Barenkamp, Stephen J TITLE OF INVENTION: High Molecular Weight Surface Proteins	WINDE OF INVENTION: OI NO. 6218141-1YPeable Haemophilus NOTHER OF SEQUENCES: 10	KKESEVONDENCE ADDRESS: ADDRESSEE: Shoemaker and Mattare, Ltd. STRREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza	STREET: Bldg. 1 CITY: Arlington	: Virginia RY: U.S.A.	22202-0286 R READABLE FORM:	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	TING SYSTEM: PC-DOS/MS-DOS 7ARE: Patentin Release #1.0, Version #1.30	: 3/08/719,641	FILING DATE: CLASSIFICATION: 530	REPLICATION DATA: (CATION NUMBER: US 08/302,832	NO LALE: 10-SEF-1594 INDELICATION DATA: DAM/ITED 2/00166	CALLON NUMBER: US FC1/USSS/UZIEG DATE: 16-MAR-1993		X/AGENT INFORMATION: Berkstresser, Jerry W	REGISTRATION NUMBER: 22,651 REFRENCE/DOCKET NUMBER: 1038-625	MUNITATION INFORMATION: HHONE: (703) 415-0810	ON FOR SEQ ID NO: 9: C CHARACTERISTICS:	LENGTH: 1338 amino acids TYPE: amino acid	STRANDEDNESS: single TOPOLOGY: linear	5-08-719-641-9 Query Match 6.1%; Score 257.5; DB 3; Length 1338; Best Local Similarity 22.0%; Pred. No. 1.8e-10;	Conservative 104	r r		631 GSIINIAGNLTVSKGANLQAITNYTFNVAGSFDNNGASNISIARGGAKFKDINNTSSL (

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1483 GINIISENGRNTVRLRGKEIDVKYIQPGVASVEEVIEAKRVLEKVKDLSDEBRETLAKLG 1542
  --SGN---VTAKTSSSVNITGDLNTIN 1482
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                                                        675 G----ATAGKATVEIVQETIAIKSVNFKPVQTENFVEKKINIGTVLELEKSNLDDIVK-G 729
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                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08728470

Patent No. 5928651

GENERAL INFORMATION:
APPLICANT:
PATELE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: Of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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APPLICATION NUMBER: US/08/728,470
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6.0%; Score 251.5; DB 2;
Best Local Similarity 22.5%; Pred. No. 6.3e-10;
Matches 188; Conservative 121; Mismatches 345;
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PRIOR PAPLICATION DATA:
APPLICATION DATA:
PELING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 69 205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAMME: BETKETESSST, JETTY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1038-633
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OPERATING SYSTEM: PC-DOS/MS-DOS
        1441 KLDGAASGDRTVVNATNASG--
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 415-0810
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 1529 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     991 SQK-EGNLTIS-----SDKWNITNQITIKAGVEG------------------ 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .019 --GRSDSSEA-----ENANLTIQTKEL-KL-AGDLNISGFNKAEITAKNGSDLTIGN 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1122 OG7 ASGGNADAKKVTFDKVKDSKISTDGHNVTLNSEVKTSNGSSNAGNDNSTGLTISAK---- 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1168 TIKGNITSONVTVTATENLVTTENAVINA-----TSGTVNISTKTGDIKGGIESTSGN 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1123 ----DV---TVNNNVTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAQNG----- 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         949 NITINSDITYR-----TIIKGNISNKSGDLNI----IDKKSDAEIQIGG-NI 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 KYGKKDNAQAYVTDVKVSEPTKLTLTGTGLDKLSADDVTLEGDKAVAIEASTDGTSAVVT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 KGNADVEYLNLANHDVKFVANNLDGSPANIF--EGGEATSTTGKLAVGIKQGDYKVEVQV 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 TKRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDFALNSQNLV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      512 GDPFGANTAAIKEVLPKTG------VVAEGGLDVVTTDSGSIGTKTIGVTGNDVGEG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   891 GSIINIAGNLTVSKGANLQAITNYTFNVAGSFDNNGASNISIARGGAK--FKDINNTSSL 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 PVDENAQPSFKDAKNIWSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 KDKVNGELVTTFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 LGGKVAPNKDLTV-KVKNQSFVT----KFVYEVKKLAVEKLTFDDDRAGQAIAFKLNDE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGEKASLNKL-VATIAGEDKVVDPGSISIKSSNHGIISVVNNYITAEAAGEATLTIKVGD 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 VIXDVK-------FKVTTDSRKLVSVKANPDKLQVVQNKTLPVT--FVTTDQY 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             563 TVHFQNGNGATLGSLYVNVTEGNVAFKNFELVSKVGQYGQSPDTKLDLNVST-TVEYQLS 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KY----TSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVTGKTPGKVDIH---LTKN 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ITGKPDGTYGPTESIDRASAAVIFTKILN---L 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.1%; Score 257.5; DB 2; Best Local Similarity 22.0%; Pred. No. 2.4e-10; Matches 183; Conservative 104; Mismatches 328;
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
ATTOREY/ABRI INFORMATION:
REGISTRATION NUMBER: 22,651
REFRENCE/DOCKET NUMBER: 22,651
REFRENCE/DOCKET NUMBER: 1038-557
TELECHONE: (703) 415-0810
INFORMATION POR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1599 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 GSI----NYLVDKGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.0%; Score 251.5; DB 3; Best Local Similarity 22.5%; Pred. No. 6.3e-10; Matches 188; Conservative 121; Mismatches 345;
                 CLASSIFICATION: 530
PRIOR APPLICATION 194A:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTONEY/APPLICATION NUMBER: 22,651
REPERENEE/DOCKET NUMBER: 22,651
REPERENEE/DOCKET NUMBER: 22,651
REPERENEE/DOCKET NUMBER: 22,651
REPERENEE/DOCKET NUMBER: 1038-625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 GSINYLVDKGAITGKPDGTYGPTE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1529 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                     993 LTIGNASGGNADAKKVIFDKVKDSKISTDGHNVTLNSEVKTSNGSSNAGNDNSTGLTISA 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                            1099 -----TIKGNITSQNVTVTATENLVTTENAVINA------TSGTVNISTKTGDIKGGIE 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      617 BYQLSKY----TSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVTGKTPGKVDIH-- 670
                                                                                                                               943 IXAGVEGGRSDSSEA-----BNANLTIQTKEL-KL-AGDLNISGFNKAEITAKNGSD 992
                                                                                                                                                                                                                                                                                   286 KLNDEKGNADVEYLNLANHDVKFVANNLDGSPANIF--EGGEATSTTGKLAVGIKOGDYK 343
                                                                                                                                                                                                                                                                                                                                                                                 344 VEVQVTKRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDFALN 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SONLVVGEKASLNKL-VATIAGEDKVVDPGSISIKSSNHGIISVVNNYITAEAAGEATLT 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 IKVGDVTKDVK------FKVTTDSRKLVSVKANPDKLQVVQNKTLPVT--FV 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTDQYGDPFGANTAAIKEVLPKTG------VVAEGGLDVVTTDSGSIGTKTIGVTGN 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LTKNG----ATAGKATVEIVQETIAIKSVNFKPVQTENFVEKKINIGTVLELEKSNLDD 725
                                                                                           DK---KYGKKDNAQAYVTDVKVSEPTKLTLTGTGLDKLSADDVTLEGDKAVAIEASTDGT 231
115 NLKDKVNGELVTTFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALT 174
                                        888 TOKTIINGNITNEKGDL---NIKNIKADABIOIG----GNISQKEGNLIISSDKVNITNQIT
                                                                                                                                                                                       232 SAVVILGGKVAPNKDLTV-KVKNQSFVT----KFVYEVKKLAVEKLTFDDDRAGQAIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              726 IVK-GIN------LIKETQHKVRVVKSG---AEQGKLYLDRNGDAVFNAGD 766
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Patent No. 6218141

GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
CORRESPONDENCE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22202-0286

MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/719,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22202-0286
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US-08-719-641-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404
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199 TKTGDINGKVESSSGSVTLVATGATLAVGNISGNTVTITADSGKLTSTVGSTINGTNSVT 1258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .147 STSGNVNITASGNTLKVSNITGODVTV-----TADAGALTTTAGSTISATTGNANIT 1198
38;
                                                                                                                               834
                                                                                                                                                                                                                                                              887
                                                                                                                                                                                                                                                                                                                                 115 NLKDKVNGELVTTFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAQFIALT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           943 IXAGVEGGRSDSSEA-----ENANLTIQTKEL-KL-AGDLNISGFNKAEITAKNGSD 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 KLNDEKGNADVEYLNLANHDVKFVANNLDGSPANIF--EGGEATSTTGKLAVGIKQGDYK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 VEVQVTKRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDFALN 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKVGDVTKDVK-----PKVTTDSRKLVSVKANPDKLQVVQNKTLPVT--FV 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           558 DVGEGTVHFQNGNGATLGSLYVNVTEGNVAFKNFELVSKVGQYGQSPDTKLDLNVST-TV 616
                                                            SIDRASAAVIFTKILNLPV
                                                                                                      DENAQPSFKDAKN1---WSSKYIAAVE-KAGVVKGDGKENFYPEGKIDRASFASMLVSAY
                                                                                                                                                                                                                                                              835 DSTFKGEASDNLNITGTFTNNGTANINIKQGVVKLQGDIN--NKGGLNITTNAS----G
                                                                                                                                                                                                                                                                                                                                                                            175 DK---KYGKKDNAQAYVIDVKVSEPIKLILIGIGLDKLSADDVILEGDKAVAIEASIDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-----DV---TVNNNVTSHKTINISAAGNVTTKEGTTINATTGSVEVTAQNG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 SAVVTLGGKVAPNKDLTV-KVKNQSFVT----KFVYEVKKLAVEKLTFDDDRAGQALAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQNLVVGEKASLNKL-VATIAGEDKVVDPGSISIKSSNHGIISVVNNYITAEAAGEATLT
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116 L-KDKVNGELVTTFEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALT 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
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GRGANISM: Haemophilus influenzae
JS-09-377-155-33
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US-09-377-155-33
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LENGTH: 2353
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                                                             ----SGN----VTAKTSSSVNITGD 1408
                                                                                                                                             1409 LNTINGLNIISENGRNTVRLRGKEIDVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERET 1468
                                                                                                     -LIKNG----ATAGKATVEIVQETIAIKSVNFKPVQTENFVEKKINIGTVLELEKSNLDD 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 DENAQPSFKDAKNI---WSSKYIAAVEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYN 115
                        617 BYQLSKY----TSDRVYSDPBNLEGYBVESKNLAVADAKIVGNKVVVTGKTPGKVDIH-- 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----EGDINNKGGLNITTNASG 957
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                                                                                                                                                                                                               ---LIKETQHKVRVVKSG---AEQGKLYLDRNGDAVFNAGD 766
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                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-APR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                             1367 NAKDAKLDGAASGDRTVVNATNASG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Berketresser, Jerry W
REGISTRATION NUMBER: 22,651
TELESTERNEC/POCKET NUMBER: 1038-557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNBER: US/08/617,697
01-APR-1996
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08617697
Patent No. 5977336
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: UK
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STRANDEDNESS: single
TOPOLOGY: linear
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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US-08-617-697-10
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1538 1169 -----TIKGNITSQNVTVTATENLVTENAVINA-----TSGTVNISTKTGDIKGGIE 1216 1269 TKTGDINGKVESSSGSVTLVATGATLAVGNISGNTVTITADSGKLTSTVGSTINGTNSVT 1328 1384 ----SGN----VTAKTSSSVNITGD 1478 958 TQKTIINGNITNEKGDL--NIKNIKADAEIQIG---GNISQKEGNLTISSDKVNITNQIT 1012 1123 K-----bV---TVNNNVTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAONG--- 1168 217 STSGNVNITASGNTLKVSNITGQDVTV-----TADAGALTTTAGSTISATTGNANIT 1268 1063 LTIGNASGGNADAKKVTFDKVKDSKISTDGHNVTLNSEVKTSNGSSNAGNDNSTGLTISA 1122 558 DVGEGTVHFQNGNGATLGSLYVNVTEGNVAFKNFELVSKVGQYGQSPDTKLDLNVST-TV 616 617 EYQLSKY----TSDRVYSDPENLEGYEVESKNLAVADAKIVGNKVVTGKTPGKVDIH-- 670 671 -LTKNG----ATAGKATVEIVQETIAIKSVNFKPVQTENFVEKKINIGTVLELEKSNLDD 725 286 KINDEKGNADVEYLNLANHDVKFVANNLDGSPANIF--EGGEATSTIGKLAVGIKQGDYK 343 175 DK---KYGKKDNAQAYVIDVKVSEPTKLTLTGTGLDKLSADDVTLEGDKAVAIEASTDGT 231 344 VEVQVTKRGGLTVSNTGIITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDFALN (479 INTINGINIISENGRNTVRLRGKEIDVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERET 232 SAVVTLGGKVAPNKDLTV-KVKNQSFVT----KFVYEVKKLAVEKLTFDDDRAGQAIAF 463 IKVGDVTKDVK------FKVTTDSRKLVSVKANPDKLQVVQNKTLPVT--FV 507 ITDQYGDPFGANTAAIKEVLPKTG------VVAEGGLDVVTTDSGSIGTKTIGVTGN 404 SQNLVVGEKASLNKL-VATIAGEDKVVDPGSISIKSSNHGIISVVNNYITAEAAGEATLT ----LIKETQHKVRVVKSG---AEQGKLYLDRNGDAVFNAGD 766

us-09-844-281-1.rai

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GENERAL INFORMATION:
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                                                                                                                81 VEKAGVVKGDGKENFYPEGKIDRASFASMLV--SAYNLKDKVNGELVTTFEDLLDHWGEE 138
                                                                                                                                                                         139 KANI--LINLGISVGTGGKWEPNK--SVSRAEAAQFIALTDKKYGKKDNAQAYVTDVKVS 194
                                                                                                                                                                                                                                                      -ATTLTEPSAGA-KSSHVDLNVDATKKSNAASIE-----DVLRAGWNIQGNGN---- 897
                                                                                                                                                                                                                                                                                                                                                                              925 KADGKGADVKIGAKTSVIKDHNGKLFTGKDLKD-----ANNGATVSEDDGKDTGTGL 976
                                                                                                                                                                                                                                                                                                                                                                                                          362 ITVKNL-----DTPASAIKNVVFALDADNDGVVNYGSKLSGKD---- 399
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                                                                                                                                                                                                                                  EPTKLTLTGTGLDKLSADDVTLEGDK---AVAIEASTDGTSAVVTLGGKVAPNKDLTVKV 251
                                                                                                                                                                                                                                                                                         KNOSFVTKFVYEVKKLAVEKLIFDDDRAGQAIAFKLNDEKGNADVEYLNLANHDVKFVAN 311
                                                                                                                                                                                                                                                                                                                     898 -NVDYVATY-----DTVNFTDDSTGTTTV-----------TVTQ 924
                                                                                                                                                                                                                                                                                                                                                 312 NLDGSPANIFEGGEAT---STTGKLAVGIKQGDYKVEVQVTKRGGLTVS-----NTGI 361
                                                                            23 DKGAIIGKPDGTYGPTESIDRASAAV--IPTKILNLPVDENAQPSFKDAKNIWSSKYIAA
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                              269;
5.9%; Score 249.5; DB 3; Length 2353; 22.0%; Pred. No. 1.7e-09; ive 107; Mismatches 335; Indels 269;
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LNGIASTLTDTL 1488
                              Conservative
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                Similarity
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   Query Match
               Best Local
Matches 20
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Sequence 4, Application US/08913942 Patent No. 6200578

RESULT 12 US-08-913-942-4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---DTPASAIKNVVFALDADNDGVVNYGSKLSGKD---- 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               852 -ATTLTEPSAGA-KSSHVDLNVDATKKSNAASIE-----DVLRAGWNIQGNGN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 DKGAITGKPDGTYGPTESIDRASAAV--IFTKILNLPVDENAQPSFKDAKNIWSSKYIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         705 DRGKVTVK-DAT---ANDADKKVATVKDVATAI-----NSAATFVKTENLTTS----
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APPLICANT: St. Geme, Joseph
APPLICANT: St. Geme, Joseph
TITLE OF INVENTION: HERMOPHILUS ADHESION PROTEINS
TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hohbach Test Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OFFMAINGS YSTEM: TC-LUCS/MS-LUCS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,942
FILING DATE: 29-DEC-1997
CLASSIFICATION S14
PROOR APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
PRILING DATE: 22-MAR-1995
ATPONEY AGENT INFORMATION:
REPERRATION NUMBER: S7.054
ATFORNEY/AGENT INFORMATION:
NAME: Vance, Dolly A.
REGISTRATION NUMBER: 39.054
REFERENCE/DOCKET NUMBER: 39.054
REFERENCE/CONTINUENTION: 1NFORMATION:
TELECOMMULCATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            898 -NVDYVATY-----DTVNFTDDSTGTTTV---
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 398-3249
                                                                                                                                                                                                                                                                                    COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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Qy 81 VEKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKVN	Db 749IDEDNPTDNGKDDALKAGDTLTFKAGKNILKVKRI		Qy 195 EPTKLTLTGTGLDKLSADDVTLEGDKAVALEASTDGTSA	Db 852 -ATTLTEPSAGA-KSSHVDLNVDATKKSNAASIEDV Oy 252 KNGSFVTKFVYEVKKLAVEKLTPDDDRAGQAIAFKLNDEKGNA	80 90 80	Qy 312 NLDGSPANIFEGGEATSTICKLAVGIKQGDYKVEVQVTKE	Cy 362 ITUKNLDTPASAIRNVVFALDADNI	Db 977 VTAKTVIDAVNKSGWRVTGBGATAETGATAVNAGNA Qy 400 -FAINSQNLVVGBKASLNKLVATIAGE	Db 1030 TATVSKDNGNINVKYDVNVGDGLKIGDDKKIVADTTTLTVTGG	Qy 441HGIISVVNNYITABAAGBATLIKVGDVTKI	488	bb 1143 SEKDFTYSLQDFLTGLTSITLGGTANGRNDTC	QY 547 IGTKTIGVTGNDVGEGTVHFQNGNGATLGSLYVNV	593	1250	Qy 644 NLAVADAKIVGNKVVVTGKTPGKVDIHLTKNGATAGKATVEIN	697	1357 DKKKVATVGDVAKAIN	OY (42 VVESGABÇLEKI ELIKURAKEDAV KINAKEDAV KINAKEDAV KINAKEDAV KINAKEDAV KINAKEDAT KINAKEDAV KINAKEDAT KINAKEDAV KINAKEDAT KINAKEDA	782		RESULT 14 US-09-797-862-33 ; Sequence 33, Application US/09797862	; Patent No. 6607729; ; GENERAL INFORMATION: ; APPLICANT: PERK, IAN RICHARD ANSELM ; APPLICANT: JENNINGS, MICHAEL PAUL	; APPLICANT: MOXON, E. RICHARD ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN ; FILE REPRENCE: 065064/0134 ; CURRENT APPLICATION NUMBER: 08/09/797,862	FILING DATE:
Db 977 VTAKTVIDAVNKSGWRVTGEGATAETGATAVNAGNAETVTSGTSVNFKNGNAT 1029	QY 400 -FALNSQNLVVGEKASLNKLVATIAGEDKVVDPGSISIKSSN 440	441HGIISVVNNYITABAAGBATLIIIKVGDVTKDVKFKVTTDSRKLVSVK-	Db 1090 VNAECLATALMNLSWTAKADKYADGESEGETDQEVKAGDKVTFKAGKNLKVKQ 1142	QY 488 ANPDKLQVVQNKTLPVTFVTTDQYGDPFGANTAAIKEVLPKTG-VVAEGGLDVVTTDSGS 546 1143 SEKDFTYSLQDTLTGLFSITLGGTANGRNDTGTVINKDGLTITLANGAA 1191	547 IGTTIIGVIGNDVGEGTVHFQNGNGATLGSLYVNVTEGNVAFKNFE	Db 1192 AGTDASNGNTISVTKDGISAGNKEITNVKSALKTYKDTQNTADETQDKEFHAAVKNAN 1249 Qy 593 LVSKVGQYGQSPDTKLDLNVSTTVEYQLSKYTSDRVYSDPENLEGYEVESK 643	Db 1250 EVEFUGKNGATVSAKTDNNGKHTVTIDVAEAKVGDGLEKDTDGKIKLKVDNTDGN 1304	OY 644 NLAVADAKIVGNKVVUTGKIPGKVDIHLITKNGATAGKATVEIVQETIAIKSVN 696	OY 697 - FKPVQTENFVEKKIN-IGTVLELEKSNLDDIVKGINLTKETQHKVR 741	Db 1357 DKKKVATVGDVAKAINDAA†FVKVENDDSATIDDSPTDDGANDALKAGDTLTLKAGKNLK 1416 Ov 742 VVKGGAFOCKIVI,DNGDADVFNAGNVK-I.GNVWVGOTGRGA 781	1417 VKRDGKNITFALANDLSVKSATVSDKLSLGTNGNKVNITSDTKGLNFAKDSKTGDDANIH	Qy 782 LPNFKADLYDTL 793	Db 1477 LNGIASTLTDTL 1488	RESULT 13 US-09-669-974-33 : Sequence 33. Application US/09669974	Patent No. 6333173 GENERAL INFORMATION:		TITLE OF INVENTION, NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128 CURRENT APPLICATION NUMBER: US/09/669,974	CURRENT FILING DATE: 2000-09-26 PRIOR APPLICATION NUMBER: US 09/377,155	PRIOR FILING DAIE: 1999-108-19 PRIOR APPLICATION NUMBER: PCT/AU98/01031 PRIOR FILING DATE: 1998-12-14	PRIOR APPLICATION. NUMBER: GB 9726398.2 PRIOR FILING DATE: 1997-12-12	NUMBER OF SEQ ID NOS: 33	i SEU ID NO 33 i LENOTH: 2353 i TYPE: PRT i CRGANIEN Haemophilus influenzae	Query Match Best Local Matches 20	AITGKPDGTYGPTESIDRASAAV-IFTKILNLPVDENAQPSFKDAKNIWS:	

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TG-VVAEGGLDVVTTDSGS 546
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NERGKVVVKGSNGATATET 1356
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NDALKAGDTLTLKAGKNLK 1416
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NAETVTSGTSVNFKNGNAT 1029
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NTADETQDKEFHAAVKNAN 1249
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DVLRAGWNIQGNGN---- 897
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VNGELVŢTFEDĻLDHWGEE 138
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RDGKNITF--DLAKNLEVK 797
                                                         KKYGKKDNAQAYVTDVKVS 194
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                                                                                                                 AVVTLGGKVAPNKDLTVKV 251
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KNQSFVTKFVYEVKKLAVEKLTFDDDRAGQAIAFKLNDEKGNADVEYLNLANHDVKFVAN 311
                                                                                                                                                                                                                                                              APPLICANT: LOOSMORE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REPERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT APPLICATION NUMBER: US/09/268,347
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 47
LENGTH: 2354
TYPE: PRT
CRORDANISM: Haemophilus influenzae
US-09-268-347-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 NLDGSPANIFEGGEAT---STTGKLAVGIKQGDYKVEVQVTKRGGLTVS-----NTGI
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                                                                                                                                                                                                          Sequence 47, Application US/09268347
Patent No. 6335182
GENERAL INFORMATION:
                                                                                                           LNGIASTLTDTL 1488
                                                                     782 LPNFKADLYDTL
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US-09-268-347-47
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Best Local S:
Matches 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          852 -ATTLTEPSAGA-KSSHVDLNVDATKKSNAASIE-----DVLRAGMNIQGNGN---- 897
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Similarity 22.0%; Pred. No. 1.7e-09;
01; Conservative 107; Mismatches 335;
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 33
                                                                                                                                                                   TYPE: PRT
ORGANISM: Haemophilus influenzae
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1250 EVEFVGKAGATVSAKTDNNGKHTVTIDVAEAKVGDGLEKDTDGKIKLKVDNTDG----N 1304
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                                                                                                                            697 -FKPVQTENFVEKKIN-IGTVLELE---KSNLDD------IVKGINLTKETQHKVR 741
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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 7, 2004, 17:29:55; Search time 18 Seconds (without alignments) 2409.691 Million cell updates/sec Run on:

Title: Perfect score:

US-09-844-281-1 4202_ 1 AGKSFPDVPAGHWAEGSINY.....IISEIGSQAVHVNVLANPNL 833 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SIAZ BACAA P94217 SIAAZ BACAA SIAAZ BACAA P94217 P49052 SIAAZ BACAA P94217 P4422 P4422 P4422 P4422 P4422 P4422 P4422 P4422 P4422 P4422 P4422 P4422 P4422 P4422 P42222 P42222 P4222 P4222 P4222 P4222 P4222 P4222 P4222 P42222 P42222 P42222 P42222 P42222 P42222 P42222 P42222 P42222 P42222 P42222 P42222 P42222 P42222 P42222	Result No.	Score	* Query Match	Length	<u> </u>	SUMMARLES	Description	ption
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ALIGNMENTS

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                                                                                     100.0%; Score 4202; DB 1; Length 862;
.larity 100.0%; Pred. No. 1.3e-175;
Consérvative 0; Mismatches 0; Indels 0
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         wall; S-layer; Complete proteome.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 120 149 180 209 240 269 VAPNKDLTVKVKNQSFVTKFVYEVKKLAVEKLTFDDDRAGQAIAFKLNDEKGNADVEYLN 300 IAPNKEL PVKVKGNTF1VKYVYEVKKLRVEOLTFDDDRADOAVVFKLNDEKGNAD1EYLD 329 360 420 1AGHDVKFVANNIDGTPANIFEGGTAESTTGKLAVGIAEGKYKVEVQVTKRGGITVSNTG 389 83 150 DGTLVTKFDDLRGHWGEEKANILVNLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYAK STRAIN=NM 105;
MEDLINE=97082965; PubMed=8964497;
Zhu X., McVeigh R.R., Malathi P., Ghosh B.K.;
"The complete nucleotide sequence of the Bacillus licheniformis NM105 1 AGKSFPDVPAGHWAEGSINYLVDKGAITGKPDGTYGPTESIDRASAAVIFTKILNLPVDE 30 AGKSFPDVPAGHWAEDSINYLVDKGAIVGKPDGTYGPTESIDRASAAVIFTKILNLPVDE 90 NAQPSFKDAKNLWSSKYIAAVEKAGVVKGDGKDNFYPEGKIDPRASFASMLVGAYNLKEKV NGELVTTPEDLLDHWGEEKANILINLGISVGTGGKWEPNKSVSRAEAAQFIALTDKKYGK 210 PENSDAKVINVAATEPTQLTLTGTGLNKTTAEDVTLEGNKAIALEASKDGKSAVVTLSGK IITVKNLDTPASAIKNVVFALDADNDGVVNYGSKLSGKDFALNSONLVVGEKASLNKLVA NAQPSFXDAKNIWSSKYIAAVBKAGVVKGDGKENFYPEGKIDRASFASMLVSAYNLKDKV KDNAQAYVTDVKVSEPTKLTLTGTGLDKLSADDVTLEGDKAVAIEASTDGTSAVVTLGGK LANHDVKFVANNLDGSPANI FEGGEATSTTGKLAVGI KQGDYKVEVQVTKRGGLTVSNTG S-layer-encoding gene.";
Gene 173:189-194(1996).
-!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly of proteins which cost the surface of bacteria.
-!- SUBCELLULAR LOCATION: Cell wall.
-!- SIMILARITY: Contains 3 S-layer homology (SLH) domains. Gaps 23; DB 1; Length 874; Indels Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1402; EFADCA4FF27D32AF CRC64; 67.4%; Score 2833.5; DB 1; 67.3%; Pred. No. 3.6e-116; iive 98; Mismatches 156; 01-NOV-1997 (Rel. 33, Last sequence update)
S-layer protein precursor (Surface layer protein)
Bacillus licheniformis. POTENTIAL. S-LAYER PROTEIN. SLH 1. EMBL, U38842; AAC44405.1; -.
PIR; JC4930; JC4930.
InterPro; IPR001119; SLH.:
Pfam; PP00395; SLH; 3.
Signal; Cell wall; S-layer; Repeat.:
SIGNAL SLH 92734 MW; Matches 569; Conservative (Rel. 33, (Rel. 33, (Rel. 35, 31 8 33 94 1 156 2 874 AA; Similarity FROM N.A. 01-FEB-1996 01-FEB-1996 01-NOV-1997 DOMAIN SEQUENCE 61 121 181 270 330 241 361 301 Query Match Local DOMAIN ò

RESULT 2 PACLI SLAP_BACLI

PRT; STANDARD;

874 AA

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

April 7, 2004, 17:29:55 ; Search time 18 Seconds (without alignments) 2409.691 Million cell updates/sec Run on:

US-09-844-281-1

4202 1 AGKSFPDVPAGHWAEGSINYITSEIGSQAVHVNVLNNPNL 833 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

141681

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SLAP BACST P2P LACLC	YPJA ECOLI MSP1 PLAFC MSP1 PLAFF	SLP1_CLOTM OMPA_RICCN ANCA_CLOTM P1P_LACLC	SLAP CAUCR BCA_STRAG
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Cell wall; S-layer; Complete proteome.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its worken by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                        STRAIN=NM 105;
MEDLINB=97082965; PubMed=8964497;
MEDLINB=97082965; PubMed=8964497;
MEDLINB=97082965; PubMed=8964497;
MEDLINB=97082965; PubMed=86quence of the Bacillus licheniformis NM105
S-layer-encoding gene.";
Gene 173:189-194 (1996).
-!- PUNCTION: The S-layer is a paracrystalline mono-layered assembly of proteins which coat the surface of bacteria.
-!- SUBCELLULAR LOCATION: Call wall.
-!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.4%; Score 2833.5; DB 1; Length 874; 67.3%; Pred. No. 3.6e-116; indels 23; ive 98; Mismatches 156; Indels 23;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
3-layer protein precursor (Surface layer protein).
Bacilius licheniformis.
Bacteria, Firmicutes; Bacillales; Bacillasea; Bacillus.
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InterPro; IPR001119; SLH.
Pfam; PF00395; SLH; 3.
Signal; Cell wall; S-layer; Repeat.
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RESULT 2 RESULI SLAP BACLI

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